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CERTIFICATE OF TRANSLATION

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THAT I translated the document identified as the Certificate of the French
National Institute of Industrial Property and of the certified true copy of the
French Patent Application No. 01 17088 filed at the National Institute of Industrial
Property on 31st December 2001, from French into English;

THAT the attached English translation is a true and correct translation of
French Patent Application No. 01 17088

to the best of my knowledge and belief; and

THAT all statements made of my own knowledge are true and that all
statements made on information and belief are believed to be true and further,
that these statements are made with the knowledge that wilful false statements
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JOHN CHARLES McGILLEY

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PRIORITY DOCUMENT**

A

FRENCH REPUBLIC
NATIONAL INSTITUTE OF INDUSTRIAL PROPERTY

PATENT OF INVENTION

UTILITY CERTIFICATE - CERTIFICATE OF ADDITION

OFFICIAL COPY

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Drawn up in Paris 11th March 2005

For the Director General of the
National Institute of Industrial
Property

The Head of the Patent
Department

[signed]
Martine PLANCHE

INPI
National Institute
of Industrial Property26 bis, rue de Saint Petersburg
75800 Paris Cedex 08
Tel: 01 53 04 53 04 Fax: 01 42 94 86 54**PATENT OF INVENTION**Intellectual Property Code – Book VI
REQUEST FOR GRANT

Delivery of documents 31 DEC 2001	Chantal PEAUCELLE
National Registration No. 0117088	Cabinet ARMENGAUD AINE
Department of filing: 75	3, Avenue Bugeaud
Date of filing 31 DEC 2001	75116 PARIS
	France
Your references for this file: CP60.558-1343	

1 NATURE OF APPLICATION		
Patent application		
2 TITLE OF INVENTION		
MEANS FOR IDENTIFYING NEISSERIA MENINGITIDIS-SPECIFIC GENES		
3 DECLARATION OF PRIORITY OR REQUEST FOR BENEFIT FROM THE FILING DATE OF A PREVIOUS FRENCH APPLICATION	Country or organization	Date
	No.	
4-1 APPLICANT		
Name	INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (I.N.S.E.R.M.)	
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6 ATTACHED DOCUMENTS AND FILES	Electronic file	Pages
		Details

received 23/07/03

B

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Request for utility certificate
resulting from an automatic conversion of the patent application
(article R. 612-55 of the Intellectual Property code)

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of Industrial Property**

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PATENT OF INVENTION

Intellectual Property Code – Book VI
REQUEST FOR GRANT

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6 ATTACHED DOCUMENTS AND FILES		Electronic file	Pages Details

1st filing
C

Description	desc.pdf.	8	
Claims	√	2	10
Drawings		142	3 fig., 3 ex.
Abstract	√	1	
Sequence listing			
Search report			
Cheque		1 doc.	0001560
7 METHOD OF PAYMENT			
Method of payment	Remittance of cheque		
Cheque No.	0001560		
8 SEARCH REPORT			
Deferred establishment			
9 FEES ATTACHED	Currency	Rate	Quantity
062 Filing	FRF	250.00	1.00
063 Search report (S.R.)	FRF	2100.00	0.00
Total to pay	FRF		250.00
10. SIGNATURE OF APPLICANT OR REPRESENTATIVE			
Signed by	Chantal PEAUCELLE		

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Means for identifying *Neisseria meningitidis*-specific genes.

The invention relates to means for identifying genes specific to *Neisseria meningitidis* (Nm in abstract). It also relates to these genes and their biological applications.

Nm is a strictly human bacteria which does not survive in the external environment. It's only known reservoir is the nasopharynx of humans. In certain circumstances which are still little understood, this bacteria will leave the nasopharynx, infiltrate the blood in circulation and cause septicaemia and/or meningitides. The existence of a meningitis suggests that the bacteria crosses the blood-brain barrier, one of the most difficult barriers to cross in the organism. *Neisseria meningitidis* is a bacteria having extracellular multiplication, in other words its dissemination in vivo is accompanied by a multiplication in the interstitial area. Very few bacteria having extracellular multiplication are capable of crossing the blood-brain barrier after the neonatal period, they are essentially *Streptococcus pneumoniae*, *Haemophilus influenzae* and *Neisseria meningitidis*. This property thus suggests specific attributes which allow these microorganisms to cross this barrier.

Neisseria meningitidis presents two specificities for a bacteria having extracellular multiplication:

(i) It is responsible for substantial bacteremia with a high number of bacteria in the blood. Thus, the comparison, in an animal model using the new-born rat, of the level of bacteremia induced by the injection of the same number of bacteria belonging to two different species (*Neisseria meningitidis* and *Klebsiella pneumoniae*) shows that *N. meningitidis* induces a bacteremia which can be 50-100 times greater than that induced by *K. pneumoniae*. This underlines the perfect adaptation of *N. meningitidis* to growth in the extra-cellular area. Certain bacterial attributes have already been identified as participating in this extracellular growth. These are essentially the polysaccharidic capsule, the lipooligosaccharide and the iron capture systems. The two first attributes allow resistance to the complement and to phagocytosis by the granulocytes and the third attribute allows the bacteria to obtain the iron essential for its growth.

(ii) The second particularity of *N. meningitidis* is related to its ability to cross the blood-brain barrier. This property results from an interaction with the cerebral endothelial cells. Until now the only bacterial attribute identified as being involved in the interaction of *N. meningitidis* at the cerebral endothelium level are the type IV pili. A molecule which is one of these pili called PilC, involved in this interaction, is the adhesin of the pili.

The inventors work has concerned the search for means allowing identification of the genes of Nm which are capable of growing specifically in serum and of crossing the blood-brain barrier.

The application to Nm of the technique described by Pelicic et al, 2000 for building a bank of mutants allowed mutagenization of more than 70% of the mutagenizable and thus non essential genes.

This tool has proved to be particularly valuable for detecting in an exhaustive fashion all of the mutants for a given phenotype, for example those which are important for growth in the serum, and for identifying adhesins which are important for interaction with the endothelial cells and thus the crossing of the blood-brain barrier and this is without necessarily testing the mutants individually for this phenotype.

Therefore the invention relates to the use of such a bank for detecting genes of Nm expressing a particular phenotype.

It also relates to the genes involved in such a phenotype.

The invention also relates to the exploitation of the thus-identified genes as Nm anti-pathogenicity targets.

It also relates to the use of the genes coding for adhesins to allow therapeutic ingredient to pass through the blood-brain barrier.

The invention moreover relates to the essential genes of *N. meningitidis*, and their homologues in other bacterial species and their use as targets for developing antibiotics.

According to the invention, genes of pathogenic bacteria, in particular of Nm, are detected, expressing a desired phenotype, according to a method characterized in that :

- a bank of mutants generated from a given bacterial strain is used so that at least 70 % of the non-essential genes, and in particular at least 80 %, or

even more than 90 %, are mutagenized by inserting a transposon in a reading frame,

- the mutants are then brought into contact, either individually, or in pools, with an environment, such as a medium, an animal or cells, capable of interacting with the mutant bacteria expressing the desired phenotype,

- when pools are used, the bacteria which have not reacted with the desired phenotype are recovered,

- the mutated genes of these bacteria are identified and their involvement in said phenotype is verified.

The bank of mutants is advantageously generated according to the method described by Pelicic et al. above.

The contact stage is carried out by passing on serum or an animal model *in vivo* or cells which are able to react with the bacteria expressing the desired phenotype and, when pools of mutants are used, the bacteria which have not reacted with the desired phenotype are recovered.

In order to identify the mutated genes of these bacteria and to verify their involvement in said phenotype, the mutants are organized into pools. For each mutant, the insertion sites are amplified using appropriate oligonucleotides. The amplification products are placed on a membrane made for example of nylon. The pools of mutants are placed under the conditions for which mutants are sought. Total DNA is prepared using bacteria obtained from each output pool and an amplification is carried out using oligonucleotides which served to amplify the insertion sites in the mutants of the pool. The amplification product then serves to hybridize the membranes which correspond to each pool. The mutants for which no amplification is detected are mutants for the phenotype considered. It will be observed that this technique allows the mutants in question to be retained, allowing each mutation to be retransformed in order to confirm the phenotype.

The invention also relates to the genes which give a bacteria the ability to grow or to react with a given environment such as serum, an animal model *in vivo*, cells.

These genes are characterized in that they can be obtained by the method defined above.

In particular the invention relates to the genes involved in the growth of bacteria in serum, chosen from the genes of Figure 3, identified with respect to the number of the pool of mutants of Figure 2.

Quite particularly the invention relates to the genes Nm 83 dxr, Nm 229, Nm 356, Nm 848 galU, and the genes of serogroup B, Nm 1771 and NmB 65 as novel products.

The invention also relates to the application of the genes selected in relation to the growth phenotype in serum, as anti-pathogenicity targets, which consists of inhibiting the growth of Nm *in vivo* in serum.

Other genes of great interest according to the invention are characterized in this that they are involved in the interaction with endothelial cells.

Therefore the invention also relates to the application of these genes to allow the opening of the blood-brain barrier to therapeutic ingredients, such as medicaments for Parkinson's Disease, Alzheimer's disease, antimitotics, medicaments for multiple sclerosis, antivirals, antimycotics and antibiotics.

Moreover the invention relates to the essential genes of Nm for which no mutant is present in the bank and the application of these genes as targets for developing antibiotics.

Other characteristics and advantages of the invention are given in the examples which follow and with reference to Figures 1 to 3 which represent:

- Figure 1, the list of genes presenting in the 2 sequenced strains of Nm more than 65% similarity on a proteinic base,
- Figure 2A, the list of genes for which there exists a mutant in the bank and Figure 2B the list of mutants classified into 96 pools of 48 mutants, and
- Figure 3, the list of the mutants altered in growth in the serum.

• Construction of a bank of mutants of Nm 8013

1. A bank of mutants is built from the *N. meningitidis* 8013 strain of serogroup C, operating according to the technique described by Pelicic et al, *Journal of Bacteriology*, 2000, 182: 5391-5398. A sequenced bank of 4547 mutants is obtained.

Statistically 80% of the insertions are in open reading frames since it concerns the % of coding regions in the genome of the 2 sequenced strains, namely Z2491, strain of serogroup A sequenced by the Sanger Center, and MC58, strain of serogroup B sequenced by TIGR. Therefore there are approximately 3600 mutants in open reading frames and in most cases, several insertions per gene. Taking into account the size of the genome, the mutagenesis thus concerns 93% of the mutagenizable genes.

The statistic formula allowing calculation of the probability (P) that a gene is mutated is the following:

$$P=1-e^{-n/P}$$

n: number of mutants in the bank

p: number of mutagenizable (non-essential) genes

The second number can only be estimated. But according to studies of bacteria better characterized than *Neisseria meningitidis*, it is reasonable to estimate that 350 genes are essential to the survival of the bacteria. Consequently, there would be 1750 non-essential genes in the meningococcus, 92.6 % (1619) of which should be mutated in the bank.

2. All of the insertions of this bank are sequenced according to the technique used for the sequencing of insertions, already described and published (Prod'hom *et al.* 1998. FEMS Microbiol Lett. 1858: 75-81). This technique uses a specific primer for the known sequence, in this case the transposon, and a second specific primer of a synthetic linker ligated to the reduced genomic DNA. The use of AmpliTaq Gold polymerase Perkin-Elmer is important for minimizing a non-specific hybridization of the primers.

- Determination of the essential genes.

An essential gene can be present only in a single strain. Any gene present in the two strains, the genome of which has been sequenced and for which a mutant does not exist in the bank of the invention is thus considered to be essential.

The genes present in the two strains are given in Figure 1. The nomenclature used is that of the strain Z2491 (sequenced by Sanger). The

list given in Figure 1 was obtained by performing a TblastN of each reading frame of Z2491 in MC58, then keeping all the frames of Z2491 which had a homology percentage greater than 65 %.

The list of the genes for which a mutant is present in the bank is represented in Figure 2A. The list of differential genes, i.e. those present in Figure 1 and not in Figure 2A, is high in essential genes. This list of differential genes includes genes which are homologous in other Gram-negative pathogenic bacteria, such as enterobacteria, Pseudomonas, Acinetobacter, or even certain Gram-positive bacteria. These genes constitute targets for developing broad spectrum antibiotics against these Gram-negative bacteria and broader spectrum antibiotics when these genes are homologous to certain genes of Gram-positive bacteria.

- Screening of the bank for different phenotypes.

For the screening, knowledge of the sequence of each insertion is applied. For this, the mutants are organized into pools of 48. For each mutant, the insertion sites are amplified using suitable oligonucleotides. Each amplification product is deposited on a nylon membrane. The pools of 48 mutants are then placed in the conditions for which mutants are sought. The total DNA is prepared using bacteria obtained from each output pool and an amplification is carried out using oligonucleotides which served to amplify the 48 insertion sites. The amplification product then serves to hybridize the membranes which correspond to each pool. The mutants for which no amplification is detected are mutants for the phenotype considered.

- Search for mutants important for growth in serum

As mentioned above, *N. meningitidis* is a bacteria having extracellular multiplication perfectly suited to this compartment. The invention therefore relates to identifying in an exhaustive way the attributes and the genes required for this growth.

1 - Isolation of the strains:

The wild strain 2C43 wt (positive control) and Z5463 CPS- (non-capsulated strain, negative control) are isolated on a GCB plate (agar 5g/l); the mutants produced from the strain 8013 are isolated on a GCB plate + *Kanamycin* 100 µg/µl.

5

The culture is carried out over 14 - 18 hours, at 37°C, in 5% CO₂.

2 - Serum:

10 The complemented human serum is stored at -80°C. After heating for 30 min. at 56°C, the serum is decomplicated. Growth is produced for the controls and the mutants with systematically complemented and decomplicated serum.

15 Each mutant is tested with a positive and a negative control to compare the growth curves produced on different days.

3 - Inoculum:

20 1 dose of well-isolated colonies is collected and dissociated in 5 ml of RPMI (GIBCO: RPMI 1640 medium with glutamax I; previously placed for 5-10 min. at ambient temperature before inoculation, to protect the bacteria from rapid variations of temperature). The mass of bacteria is taken up using a P1000, then vortexed. The preculture is subjected to stirring at 37 °C for 2 hours. The OD is then measured at 600 nm (the white control being RMPI) and the inoculum is returned to 0.1 in RPMI (previously placed for 5-10 min. at
25 ambient temperature).

4 - Growth medium:

98 µl of serum and 292 µl of RPMI (25% serum, 75% RMPI) is deposited per well and left for 5 min. at ambient temperature before inoculation.

30

400 µl of water is introduced into the optionally empty wells.

5 - Inoculation:

After stirring, 10 µl of inoculum adjusted to 0.1 of OD is collected, and it is deposited in a well containing growth medium, then mixed using a P1000. The wells are placed in an oven at 37°C, in 5% CO₂. The inoculum is analyzed at T0 and the bacterial growth at various times, by plating 50 µl of different dilutions on GCB plates.

6 - Sampling:

Suspension takes place again (with a P1000) before sampling at 0 hour, 1 hour, 5 hours post inoculation. 20 µl of inoculated culture medium is taken which is placed in 180 µl of RPMI (D1; tube 1.5 ml, previously placed at ambient temperature for 10 min., before sampling, in order to avoid a large difference in temperature). The mixture is vortexed.

7 - Dilutions:

The tube D1 is vortexed, then 50 µl of D1 is sampled which is added to 450 µl of RPMI (D2; 2 ml tube, previously placed at ambient temperature for 10 min.). Between each dilution stage vortexing is carried out and the cone is changed. Dilutions are carried out up to the dilution D4 for the time T0, D3 for the time T1, and D5 for the time T5.

8 - Inoculation:

The inoculation takes place on a GCB plate for the controls, and GCB+ kanamycin 100 µg/µl for the mutants. Vortexing is carried out, then 50 µl is taken from each dilution, followed by incubating upside down in an oven at 37°C, in 5% CO₂, for 14-18 hours, before counting the colonies. D4, 3 are inoculated for the time T0; D0, 1, 2, 3 for the time T1; D5, 4, 3, 2, 1 for the time T5.

9 - Counting of the number of colonies (CFI)

The growth curves (log₁₀ CFU as a function of incubation time in hours) are drawn up.

- Identification of the adhesins for endothelial cells.

The important adhesins for interaction on endothelial cells can be used to allow the opening of the blood-brain barrier and to allow medicaments to pass into the brain.

- 5 HUVEC cells at confluence are inoculated in 24-well cell culture microplates at a density of 10^5 /well. The cells are washed the following day in 10% serum/RPMI, and are incubated for 2 hours at 37°C. At the same time, the bacteria are resuspended in the same medium at an OD₅₅₀ of 0.1 to 0.01 and incubated for 2 hours at 37°C. The suspension of bacteria is used to
- 10 infect the cells for 30 min at 37°C.

The infection then continues for 4 - 5 hours with the cells being washed each hour.

CLAIMS

1/ Exhaustive method for detecting pathogenic bacteria genes, in particular Nm, expressing a desired phenotype, characterized in that :

5 - a bank of mutants generated from a given bacterial strain is used so that at least 70% of the non-essential genes, and in particular at least 80%, or even more than 90%, are mutagenized by inserting a transposon in a reading frame,

10 - the mutants are then brought into contact, either individually, or in pools, with an environment, such as a medium, an animal or cells, capable of interacting with the mutant bacteria expressing the desired phenotype,

 - when pools are used, the bacteria not having reacted with the desired phenotype are recovered,

 - the mutated genes of these bacteria are identified and their involvement in said phenotype is verified.

15 2/ Method according to claim 1, characterized in that, in the contact stage, the mutants of the bank are passed through serum.

 3/ Method according to claim 1, characterized in that, in the contact stage, the mutants of the bank are passed over endothelial cells.

20 4/ Genes which give a bacteria the ability to grow or to interact with a given environment, such as serum, an *in vivo* animal model, cells, characterized in that they can be obtained by the method according to any one of claims 1 to 3.

 5/ Genes according to claim 4, characterized in that they are involved in the growth of the bacteria in serum and are chosen from those in Figure 3.

25 6/ Genes according to claim 5, characterized in that they are chosen from Nm 83 dxr, Nm 229, Nm 356, Nm 848 galU, and the genes of serogroup B, Nm B 1771 and Nm B 65.

 7/ Genes according to claim 4, characterized in that they are involved in the interaction with endothelial cells.

30 8/ Application of the genes selected according to the method of claim 2, or according to claim 5 or 6, as anti-pathogenicity targets, which consists in inhibiting Nm growth *in vivo* in the serum.

CLAIMS

1/ Exhaustive method for detecting pathogenic bacteria genes, in particular Nm, expressing a desired phenotype, characterized in that :

5 - a bank of mutants generated from a given bacterial strain is used so that at least 70% of the non-essential genes, and in particular at least 80%, or even more than 90%, are mutagenized by inserting a transposon in a reading frame,

10 - the mutants are then brought into contact, either individually, or in pools, with an environment, such as a medium, an animal or cells, capable of interacting with the mutant bacteria expressing the desired phenotype,

 - when pools are used, the bacteria not having reacted with the desired phenotype are recovered,

 - the mutated genes of these bacteria are identified and their involvement in said phenotype is verified.

15 2/ Method according to claim 1, characterized in that, in the contact stage, the mutants of the bank are passed through serum.

 3/ Method according to claim 1, characterized in that, in the contact stage, the mutants of the bank are passed over endothelial cells.

20 4/ Nm genes, characterized in that they are chosen from dxr (1-deoxy-D-xylulose-5-phosphate reductoisomerase), galU (UTP-glucose-1-phosphate uridylyltransferase), and the gene of serotype B hisC (histidinol-phosphate amino transferase).

25 5/ Application of the genes selected according to the method of claim 2, or according to claim 4, as anti-pathogenicity targets, for the screening and manufacture of inhibitors of Nm growth in the serum.

30 6/ Application of the genes selected according to the method of claim 3, or according to claim 4, for the screening and manufacture of medicaments allowing the opening of the blood-brain barrier to therapeutic ingredients such as medicaments for Parkinson's Disease, Alzheimer's disease, antimitotics, medicaments for multiple sclerosis, antivirals, antimycotics and antibiotics.

 7/ Application according to one of claims 5 or 6, characterized in that essential genes of Nm are used as targets for the screening and manufacture of antibiotics.

9/ Application of the genes selected according to the method of claim 3, or according to claim 7, to allow the opening of the blood-brain barrier to therapeutic ingredients such as medicaments for Parkinson's Disease, Alzheimer's disease, antimitotics, medicaments for multiple sclerosis, 5 antivirals, antimycotics and antibiotics.

10/ Application of the essential genes of Nm as targets for developing antibiotics.

Z2491 orfs having more than 65 % homology with MC58

Z2491 gene	MC58 in silico
NMA0002	99
NMA0003	99
NMA0004	100
NMA0005	100
NMA0006	99
NMA0007	99
NMA0008	100
NMA0009	99
NMA0010	97
NMA0011	97
NMA0012	99
NMA0013	98
NMA0014	99
NMA0015	98
NMA0016	99
NMA0017	97
NMA0018	99
NMA0019	99
NMA0020	99
NMA0021	100
NMA0022	78
NMA0023	100
NMA0024	94
NMA0025	97
NMA0027	97
NMA0028	99
NMA0029	95
NMA0030	100
NMA0031	99
NMA0032	99
NMA0033	99
NMA0035	97
NMA0036	77
NMA0037	100
NMA0042	98
NMA0043	100
NMA0044	98
NMA0048	99
NMA0049	98
NMA0050	100
NMA0052	95
NMA0054	97
NMA0055	99
NMA0056	99
NMA0057	98
NMA0059	91
NMA0060	99
NMA0061	98
NMA0062	98
NMA0063	97
NMA0064	100

Figure 1

NMA0065	94	Figure 1 (cntd)
NMA0066	98	
NMA0067	97	
NMA0068	88	
NMA0069	98	
NMA0070	99	
NMA0071	99	
NMA0072	99	
NMA0073	100	
NMA0074	99	
NMA0075	98	
NMA0076	97	
NMA0077	98	
NMA0078	96	
NMA0079	99	
NMA0080	100	
NMA0081	99	
NMA0082	99	
NMA0083	98	
NMA0084	99	
NMA0085	99	
NMA0086	98	
NMA0087	98	
NMA0088	99	
NMA0090	99	
NMA0091	98	
NMA0092	98	
NMA0093	99	
NMA0094	98	
NMA0096	70	
NMA0098	99	
NMA0099	98	
NMA0100	99	
NMA0101	99	
NMA0102	99	
NMA0103	100	
NMA0104	100	
NMA0105	100	
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NMA0107	97	
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NMA0111	100	
NMA0112	100	
NMA0113	100	
NMA0114	99	
NMA0115	100	
NMA0116	100	
NMA0117	99	
NMA0118	100	
NMA0119	100	
NMA0120	100	
NMA0121	100	
NMA0122	100	
NMA0123	100	

NMA0124	100
NMA0125	100
NMA0126	99
NMA0127	97
NMA0128	100
NMA0129	100
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NMA0134	100
NMA0135	99
NMA0136	100
NMA0137	100
NMA0138	95
NMA0139	98
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NMA0167	98
NMA0168	100
NMA0169	97
NMA0170	99
NMA0171	98
NMA0171A	100
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Figure 1 (cntd)

NMA0185	99
NMA0186	98
NMA0187	93
NMA0188	99
NMA0189	97
NMA0190	97
NMA0191	100
NMA0193	97
NMA0194	98
NMA0195	99
NMA0196	88
NMA0197	92
NMA0198	96
NMA0203	97
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NMA0237	99
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NMA0243	97
NMA0244	96
NMA0245	97
NMA0246	98
NMA0247	98
NMA0248	96
NMA0249	97
NMA0250	97
NMA0251	94

Figure 1 (cntd)

NMA0252	100
NMA0253	98
NMA0254	99
NMA0255	98
NMA0256	97
NMA0257	98
NMA0258	99
NMA0259	97
NMA0260	98
NMA0261	97
NMA0262	97
NMA0263	99
NMA0264	91
NMA0265	90
NMA0266	86
NMA0267	87
NMA0268	86
NMA0269	86
NMA0270	83
NMA0271	66
NMA0272	66
NMA0273	98
NMA0274	95
NMA0275	98
NMA0276	98
NMA0277	95
NMA0279	98
NMA0280	98
NMA0281	99
NMA0282	99
NMA0283	98
NMA0284	97
NMA0285	96
NMA0286	91
NMA0287	99
NMA0288	99
NMA0289	100
NMA0290	99
NMA0291	98
NMA0292	98
NMA0293	85
NMA0295	99
NMA0296	98
NMA0298	98
NMA0299	83
NMA0300	96
NMA0301	100
NMA0303	99
NMA0304	97
NMA0305	99
NMA0305A	98
NMA0306	100
NMA0307	98
NMA0308	98
NMA0309	100
NMA0310	100

Figure 1 (cntd)

NMA0311	100
NMA0312	99
NMA0313	96
NMA0314	100
NMA0315	94
NMA0316	100
NMA0317	100
NMA0318	100
NMA0319	96
NMA0320	100
NMA0321	99
NMA0322	99
NMA0323	100
NMA0324	75
NMA0325	100
NMA0326	100
NMA0327	100
NMA0328	100
NMA0329	94
NMA0330	88
NMA0331	98
NMA0333	99
NMA0335	92
NMA0336	100
NMA0337	99
NMA0338	94
NMA0339	97
NMA0340	100
NMA0341	99
NMA0342	98
NMA0343	96
NMA0344	98
NMA0344A	100
NMA0345	98
NMA0346	100
NMA0347	98
NMA0348	100
NMA0349	94
NMA0350	98
NMA0351	97
NMA0353	97
NMA0354	100
NMA0356	98
NMA0357	98
NMA0358	91
NMA0360	100
NMA0361	99
NMA0362	99
NMA0363	97
NMA0364	97
NMA0365	89
NMA0366	80
NMA0367	99
NMA0368	95
NMA0369	98
NMA0370	99

Figure 1 (cntd)

NMA0371	95	
NMA0372	98	
NMA0373	97	
NMA0374	98	
NMA0375	100	Figure 1 (cntd)
NMA0376	99	
NMA0377	100	
NMA0378	100	
NMA0379	100	
NMA0380	100	
NMA0381	99	
NMA0382	99	
NMA0383	100	
NMA0384	96	
NMA0385	96	
NMA0386	97	
NMA0387	98	
NMA0388	99	
NMA0389	99	
NMA0390	99	
NMA0391	100	
NMA0392	99	
NMA0393	95	
NMA0394	94	
NMA0395	70	
NMA0396	83	
NMA0397	98	
NMA0398	93	
NMA0400	100	
NMA0401	100	
NMA0402	98	
NMA0403	97	
NMA0404	98	
NMA0405	99	
NMA0409	97	
NMA0410	99	
NMA0411	98	
NMA0412	100	
NMA0413	99	
NMA0414	99	
NMA0415	100	
NMA0416	99	
NMA0417	100	
NMA0418	99	
NMA0419	100	
NMA0420	100	
NMA0421	100	
NMA0422	98	
NMA0423	97	
NMA0424	99	
NMA0425	99	
NMA0426A	85	
NMA0430	95	
NMA0431	98	
NMA0433	99	
NMA0434	100	

NMA0435	100
NMA0436	99
NMA0437	98
NMA0438	99
NMA0439	100
NMA0440	89
NMA0441	99
NMA0442	99
NMA0444	95
NMA0445	98
NMA0447	99
NMA0448	94
NMA0449	78
NMA0450	98
NMA0451	97
NMA0452	99
NMA0453	98
NMA0454	99
NMA0455	97
NMA0456	97
NMA0457	92
NMA0458	95
NMA0459	99
NMA0461	96
NMA0462	98
NMA0463	99
NMA0464	97
NMA0465	98
NMA0466	97
NMA0467	96
NMA0468	98
NMA0470	99
NMA0471	98
NMA0472	99
NMA0473	99
NMA0476	98
NMA0477	97
NMA0478	97
NMA0480	99
NMA0483	98
NMA0485	99
NMA0486	100
NMA0487	100
NMA0488	98
NMA0489	89
NMA0490	99
NMA0491	100
NMA0492	100
NMA0493	97
NMA0494	95
NMA0495	100
NMA0496	97
NMA0497	98
NMA0498	99
NMA0499	99
NMA0501	98

Figure 1 (cntd)

NMA0502	100	
NMA0503	98	
NMA0504	98	
NMA0505	97	
NMA0506	99	Figure 1 (cntd)
NMA0507	98	
NMA0508	99	
NMA0510	97	
NMA0511	99	
NMA0512	99	
NMA0513	100	
NMA0514	100	
NMA0515	99	
NMA0516	98	
NMA0517	99	
NMA0518	99	
NMA0519	99	
NMA0520	97	
NMA0521	100	
NMA0522	96	
NMA0523	97	
NMA0524	94	
NMA0525	92	
NMA0526	78	
NMA0527	82	
NMA0528	98	
NMA0529	99	
NMA0530	100	
NMA0531	92	
NMA0532	98	
NMA0532a	95	
NMA0533	98	
NMA0534	98	
NMA0535	99	
NMA0536	97	
NMA0537	94	
NMA0538	98	
NMA0541	100	
NMA0542	98	
NMA0543	98	
NMA0544	98	
NMA0545	98	
NMA0546	98	
NMA0547	96	
NMA0548	98	
NMA0549	99	
NMA0550	97	
NMA0551	100	
NMA0552	98	
NMA0553	99	
NMA0554	91	
NMA0555	97	
NMA0556	96	
NMA0557	99	
NMA0559	93	
NMA0560	95	

NMA0561	97
NMA0562	96
NMA0563	80
NMA0564	98
NMA0565	99
NMA0567	99
NMA0568	75
NMA0569	100
NMA0570	98
NMA0571	97
NMA0572	98
NMA0573	93
NMA0574	99
NMA0575	99
NMA0576	99
NMA0577	99
NMA0578	99
NMA0579	97
NMA0580	98
NMA0581	98
NMA0582	100
NMA0583	95
NMA0584	97
NMA0585	93
NMA0586	96
NMA0587	99
NMA0588	92
NMA0589	98
NMA0590	99
NMA0591	86
NMA0592	97
NMA0594	98
NMA0595	97
NMA0596	98
NMA0597	100
NMA0598	99
NMA0599	97
NMA0600	99
NMA0601	98
NMA0602	98
NMA0605	92
NMA0607	66
NMA0608	99
NMA0609	87
NMA0611	96
NMA0612	99
NMA0613	100
NMA0614	99
NMA0615	98
NMA0616	99
NMA0617	99
NMA0618	100
NMA0619	99
NMA0620	98
NMA0621	95
NMA0622	97

Figure 1 (cntd)

NMA0623	100
NMA0624	100
NMA0625	99
NMA0626	77
NMA0627	99
NMA0632	98
NMA0632a	92
NMA0633	96
NMA0634	91
NMA0635	98
NMA0636	97
NMA0637	97
NMA0638	95
NMA0639	95
NMA0643	97
NMA0644	96
NMA0645	99
NMA0646	97
NMA0647	96
NMA0648	100
NMA0650	99
NMA0651	100
NMA0652	100
NMA0653	100
NMA0654	98
NMA0655	100
NMA0656	98
NMA0658	100
NMA0659	100
NMA0660	99
NMA0661	99
NMA0662	99
NMA0663	98
NMA0664	99
NMA0664a	100
NMA0665	98
NMA0666	99
NMA0668	100
NMA0669	100
NMA0670	97
NMA0671	77
NMA0672	99
NMA0673	98
NMA0674	99
NMA0675	99
NMA0676	97
NMA0677	93
NMA0678	96
NMA0679	97
NMA0680	100
NMA0681	96
NMA0683	97
NMA0684	100
NMA0685	100
NMA0686	100
NMA0687	93

Figure 1 (cntd)

NMA0688	78
NMA0690	66
NMA0691	100
NMA0692	98
NMA0693	99
NMA0694	100
NMA0695	70
NMA0696	95
NMA0696A	98
NMA0697	100
NMA0698	99
NMA0699	99
NMA0700	99
NMA0701	99
NMA0702	99
NMA0703	99
NMA0704	99
NMA0706	94
NMA0707	97
NMA0708	96
NMA0709	98
NMA0710	99
NMA0711	99
NMA0712	96
NMA0714	100
NMA0715	98
NMA0716	99
NMA0717	97
NMA0718	99
NMA0719	98
NMA0720	96
NMA0721	97
NMA0722	100
NMA0723	98
NMA0724	98
NMA0725	99
NMA0726	93
NMA0728	99
NMA0729	99
NMA0730	100
NMA0731	97
NMA0732	98
NMA0733	91
NMA0734	92
NMA0735	99
NMA0736	97
NMA0737	98
NMA0738	99
NMA0739	100
NMA0740	98
NMA0741	99
NMA0742	100
NMA0744	100
NMA0745	100
NMA0746	98
NMA0747	99

Figure 1 (cntd)

NMA0748	98
NMA0749	99
NMA0750	99
NMA0751	98
NMA0752	97
NMA0753	99
NMA0754	99
NMA0755	99
NMA0756	99
NMA0757	100
NMA0758	98
NMA0759	97
NMA0760	98
NMA0761	95
NMA0762	98
NMA0763	99
NMA0764	100
NMA0765	100
NMA0766	98
NMA0767	98
NMA0768	99
NMA0769	95
NMA0770	98
NMA0771	68
NMA0774	81
NMA0775	75
NMA0776	75
NMA0777	92
NMA0778	86
NMA0779	83
NMA0780	84
NMA0781	79
NMA0784	88
NMA0786	70
NMA0788	87
NMA0789	97
NMA0790	99
NMA0791	98
NMA0792	99
NMA0793	98
NMA0794	98
NMA0795	100
NMA0796	98
NMA0797	99
NMA0798	100
NMA0799	100
NMA0800	98
NMA0801	99
NMA0802	91
NMA0803	98
NMA0804	98
NMA0805	100
NMA0806	99
NMA0807	99
NMA0808	98
NMA0810	99

Figure 1 (cntd)

NMA0811	99
NMA0812	99
NMA0813	100
NMA0814	100
NMA0815	100
NMA0816	98
NMA0817	98
NMA0818	99
NMA0819	97
NMA0820	99
NMA0821	92
NMA0822	93
NMA0823	98
NMA0824	96
NMA0825	99
NMA0826	99
NMA0827	99
NMA0828	96
NMA0829	98
NMA0830	98
NMA0831	98
NMA0832	98
NMA0833	99
NMA0835	99
NMA0836	98
NMA0837	98
NMA0838	98
NMA0839	98
NMA0840	96
NMA0841	99
NMA0842	100
NMA0843	99
NMA0844	99
NMA0845	90
NMA0846	88
NMA0847	99
NMA0848	98
NMA0849	93
NMA0850	98
NMA0851	98
NMA0852	97
NMA0853	77
NMA0855	91
NMA0856	93
NMA0857	79
NMA0858	97
NMA0859	99
NMA0860	94
NMA0861	98
NMA0862	98
NMA0864	98
NMA0865	97
NMA0866	98
NMA0867	96
NMA0868	98
NMA0869	97

Figure 1 (cntd)

NMA0870	99
NMA0871	99
NMA0872	99
NMA0873	99
NMA0874	100
NMA0875	98
NMA0876	99
NMA0877	99
NMA0878	100
NMA0879	98
NMA0880	99
NMA0881	98
NMA0882	100
NMA0884	99
NMA0885	99
NMA0886	100
NMA0887	98
NMA0888	99
NMA0889	99
NMA0890	94
NMA0891	99
NMA0892	98
NMA0894	97
NMA0895	99
NMA0896	97
NMA0897	97
NMA0899	99
NMA0900	99
NMA0902	99
NMA0903	98
NMA0904	99
NMA0905	97
NMA0906	96
NMA0907	97
NMA0908	98
NMA0909	98
NMA0911	98
NMA0912	99
NMA0913	99
NMA0914	100
NMA0915	98
NMA0916	97
NMA0917	98
NMA0918	99
NMA0919	97
NMA0925	99
NMA0927	99
NMA0928	98
NMA0929	99
NMA0930	100
NMA0931	100
NMA0932	99
NMA0933	98
NMA0937	96
NMA0938	100
NMA0939	99

Figure 1 (cntd)

NMA0940	98
NMA0941	92
NMA0942	97
NMA0943	97
NMA0944	92
NMA0945	99
NMA0946	98
NMA0947	99
NMA0948	99
NMA0950	98
NMA0951	99
NMA0952	98
NMA0953	97
NMA0954	96
NMA0955	97
NMA0956	99
NMA0957	97
NMA0958	99
NMA0959	97
NMA0960	97
NMA0961	100
NMA0962	99
NMA0963	98
NMA0964	99
NMA0965	100
NMA0966	98
NMA0967	94
NMA0968	98
NMA0969	99
NMA0970	100
NMA0971	96
NMA0972	98
NMA0973	100
NMA0974	100
NMA0975	98
NMA0976	98
NMA0977	99
NMA0978	95
NMA0979	99
NMA0980	92
NMA0981	98
NMA0982	97
NMA0983	70
NMA0984	100
NMA0985	99
NMA0986	96
NMA0987	97
NMA0988	96
NMA0989	99
NMA0990	97
NMA0991	98
NMA0992	98
NMA0993	98
NMA0994	99
NMA0995	98
NMA0996	99

Figure 1 (cntd)

NMA0997	98
NMA0999	99
NMA1000	99
NMA1001	97
NMA1002	100
NMA1003	99
NMA1004	98
NMA1005	100
NMA1006	99
NMA1007	99
NMA1008	100
NMA1009	97
NMA1010	96
NMA1011	99
NMA1012	98
NMA1013	98
NMA1015	98
NMA1016	98
NMA1017	100
NMA1018	98
NMA1019	95
NMA1020	98
NMA1021	98
NMA1022	98
NMA1023	99
NMA1024	97
NMA1025	93
NMA1026	99
NMA1027	100
NMA1028	99
NMA1029	98
NMA1030	99
NMA1031	99
NMA1032	99
NMA1033	99
NMA1034	97
NMA1035	99
NMA1036	90
NMA1037	99
NMA1038	98
NMA1039	100
NMA1042	93
NMA1045	94
NMA1046	89
NMA1047	99
NMA1048	98
NMA1049	86
NMA1051	91
NMA1052	99
NMA1053	97
NMA1054	98
NMA1056	99
NMA1057	93
NMA1058	89
NMA1059	96
NMA1060	100

Figure 1 (cntd)

NMA1061	98
NMA1062	99
NMA1063	98
NMA1064	97
NMA1065	98
NMA1066	98
NMA1067	99
NMA1068	99
NMA1070	99
NMA1071	88
NMA1072	100
NMA1073	100
NMA1074	99
NMA1075	80
NMA1076	98
NMA1084	97
NMA1085	99
NMA1086	98
NMA1087	100
NMA1088	97
NMA1089	96
NMA1090	97
NMA1091	95
NMA1092	97
NMA1093	100
NMA1094	98
NMA1095	99
NMA1096	99
NMA1097	98
NMA1098	99
NMA1100	99
NMA1101	99
NMA1102	100
NMA1104	99
NMA1105	99
NMA1106	93
NMA1107	93
NMA1108	82
NMA1109	96
NMA1110	97
NMA1111	94
NMA1112	98
NMA1113	98
NMA1114	98
NMA1115	98
NMA1116	98
NMA1117	96
NMA1118	98
NMA1119	98
NMA1120	99
NMA1121	98
NMA1122	99
NMA1123	99
NMA1124	98
NMA1126	100
NMA1127	97

Figure 1 (cntd)

NMA1128	97
NMA1129	98
NMA1129a	98
NMA1130	94
NMA1131	98
NMA1132	97
NMA1133	99
NMA1134	94
NMA1135	99
NMA1136	98
NMA1137	100
NMA1138	98
NMA1139	99
NMA1140	98
NMA1141	100
NMA1142	99
NMA1143	100
NMA1144	98
NMA1145	99
NMA1146	100
NMA1147	100
NMA1148	100
NMA1149	100
NMA1150	96
NMA1151	99
NMA1152	100
NMA1153	99
NMA1154	99
NMA1159	98
NMA1160	98
NMA1161	99
NMA1162	95
NMA1163	98
NMA1164	100
NMA1165	99
NMA1166	100
NMA1167	98
NMA1168	96
NMA1169	100
NMA1170	99
NMA1171	100
NMA1172	74
NMA1173	70
NMA1174	100
NMA1175	97
NMA1176	92
NMA1177	97
NMA1178	97
NMA1179	96
NMA1180	98
NMA1181	92
NMA1182	95
NMA1183	93
NMA1185	94
NMA1186	88
NMA1187	100

Figure 1 (cntd)

NMA1188	97
NMA1189	99
NMA1190	97
NMA1191	96
NMA1192	100
NMA1193	100
NMA1194	100
NMA1195	100
NMA1196	95
NMA1197	97
NMA1198	100
NMA1199	98
NMA1200	90
NMA1201	100
NMA1202	98
NMA1203	100
NMA1204	100
NMA1205	98
NMA1206	98
NMA1207	95
NMA1208	94
NMA1212	94
NMA1217	93
NMA1218	97
NMA1219	96
NMA1220	98
NMA1221	98
NMA1222	99
NMA1223	100
NMA1224	99
NMA1230	100
NMA1231	100
NMA1232	90
NMA1233	97
NMA1234	82
NMA1237	99
NMA1239	79
NMA1242	84
NMA1243	99
NMA1244	99
NMA1245	97
NMA1246	98
NMA1247	99
NMA1249	98
NMA1250	99
NMA1251	99
NMA1252	98
NMA1253	98
NMA1254	99
NMA1255	99
NMA1256	90
NMA1257	99
NMA1258	100
NMA1259	97
NMA1260	98
NMA1261	96

Figure 1 (cntd)

NMA1262	99
NMA1263	98
NMA1264	95
NMA1265	98
NMA1266	97
NMA1267	98
NMA1268	98
NMA1270	99
NMA1272	99
NMA1273	98
NMA1274	98
NMA1275	99
NMA1276	99
NMA1278	98
NMA1279	98
NMA1280	96
NMA1281	96
NMA1284	94
NMA1285	72
NMA1286	83
NMA1301	88
NMA1302	100
NMA1303	97
NMA1304	99
NMA1305	97
NMA1306	95
NMA1307	83
NMA1308	83
NMA1309	66
NMA1310	98
NMA1311	70
NMA1312	86
NMA1313	97
NMA1314	99
NMA1315	99
NMA1316	100
NMA1318	99
NMA1319	99
NMA1320	98
NMA1321	100
NMA1322	97
NMA1323	99
NMA1324	98
NMA1325	96
NMA1326	100
NMA1327	98
NMA1328	97
NMA1329	97
NMA1330	98
NMA1331	98
NMA1332	100
NMA1334	100
NMA1335	100
NMA1336	94
NMA1338	98
NMA1339	98

Figure 1 (cntd)

NMA1340	98
NMA1341	99
NMA1343	97
NMA1344	100
NMA1345	91
NMA1347	100
NMA1348	100
NMA1349	99
NMA1350	99
NMA1351	99
NMA1353	100
NMA1354	100
NMA1355	90
NMA1356	96
NMA1357	96
NMA1358	99
NMA1359	96
NMA1360	98
NMA1361	98
NMA1362	99
NMA1363	95
NMA1364	99
NMA1365	99
NMA1366	94
NMA1367	95
NMA1368	97
NMA1369	96
NMA1370	99
NMA1371	98
NMA1372	99
NMA1373	100
NMA1374	98
NMA1375	100
NMA1376	100
NMA1377	99
NMA1378	99
NMA1379	99
NMA1380	100
NMA1381	99
NMA1382	99
NMA1383	96
NMA1384	98
NMA1385	96
NMA1390	100
NMA1391	96
NMA1393	95
NMA1394	98
NMA1395	100
NMA1396	95
NMA1397	99
NMA1398	98
NMA1400	98
NMA1401	99
NMA1402	99
NMA1403	98
NMA1404	98

Figure 1 (cntd)

NMA1405	100
NMA1406	99
NMA1407	99
NMA1408	98
NMA1409	99
NMA1410	99
NMA1411	99
NMA1412	98
NMA1413	98
NMA1414	97
NMA1415	98
NMA1416	98
NMA1417	98
NMA1418	97
NMA1419	100
NMA1420	99
NMA1421	99
NMA1423	96
NMA1424	93
NMA1425	98
NMA1427	97
NMA1429	98
NMA1430	90
NMA1432	99
NMA1433	98
NMA1437	100
NMA1438	99
NMA1439	97
NMA1440	97
NMA1441	98
NMA1442	100
NMA1443	100
NMA1444	99
NMA1445	98
NMA1446	99
NMA1447	99
NMA1448	98
NMA1449	98
NMA1450	99
NMA1451	100
NMA1452	99
NMA1453	98
NMA1454	98
NMA1456	98
NMA1457	98
NMA1459	99
NMA1460	98
NMA1461	100
NMA1462	99
NMA1463	99
NMA1464	96
NMA1465	98
NMA1466	97
NMA1468	99
NMA1469	96
NMA1470	97

Figure 1 (cntd)

NMA1471	99
NMA1472	98
NMA1473	98
NMA1474	98
NMA1475	96
NMA1476	97
NMA1478	98
NMA1479	97
NMA1480	100
NMA1481	99
NMA1482	98
NMA1483	99
NMA1484	99
NMA1485	99
NMA1486	99
NMA1487	90
NMA1488	99
NMA1489	95
NMA1490	99
NMA1491	87
NMA1492	99
NMA1493	98
NMA1494	96
NMA1495	99
NMA1496	100
NMA1497	100
NMA1498	99
NMA1499	99
NMA1500	100
NMA1501	99
NMA1503	96
NMA1504	99
NMA1505	98
NMA1506	99
NMA1507	98
NMA1508	100
NMA1509	97
NMA1514	98
NMA1515	99
NMA1516	100
NMA1517	100
NMA1518	100
NMA1519	99
NMA1520	100
NMA1521	100
NMA1522	99
NMA1523	99
NMA1524	98
NMA1525	98
NMA1526	99
NMA1527	98
NMA1528	99
NMA1529	99
NMA1531	99
NMA1532	100
NMA1533	93

Figure 1 (cntd)

NMA1534	99
NMA1535	100
NMA1536	99
NMA1537	99
NMA1538	99
NMA1539	96
NMA1540	98
NMA1541	97
NMA1542	98
NMA1543	98
NMA1545	98
NMA1546	99
NMA1547	99
NMA1548	98
NMA1549	99
NMA1550	97
NMA1551	99
NMA1552	98
NMA1553	98
NMA1554	99
NMA1555	99
NMA1556	97
NMA1557	99
NMA1558	77
NMA1559	99
NMA1560	99
NMA1561	93
NMA1562	99
NMA1563	96
NMA1564	100
NMA1565	98
NMA1566	98
NMA1567	95
NMA1568	98
NMA1569	99
NMA1570	98
NMA1571	96
NMA1572	99
NMA1573	98
NMA1574	99
NMA1575	96
NMA1576	93
NMA1577	93
NMA1578	97
NMA1579	98
NMA1580	99
NMA1581	98
NMA1582	99
NMA1583	93
NMA1584	97
NMA1585	99
NMA1586	93
NMA1588	96
NMA1589	96
NMA1591	93
NMA1592	99

Figure 1 (suite)

NMA1593	100
NMA1594	96
NMA1595	99
NMA1596	98
NMA1597	100
NMA1598	99
NMA1599	99
NMA1600	99
NMA1601	100
NMA1601a	99
NMA1601b	98
NMA1602	99
NMA1603	97
NMA1604	99
NMA1605	100
NMA1607	100
NMA1608	100
NMA1609	98
NMA1610	98
NMA1611	100
NMA1612	92
NMA1613	98
NMA1614	99
NMA1615	99
NMA1616	100
NMA1617	99
NMA1618	95
NMA1619	98
NMA1620	99
NMA1621	100
NMA1622	99
NMA1623	99
NMA1624	99
NMA1625	85
NMA1626	86
NMA1627	98
NMA1628	97
NMA1629	99
NMA1630	98
NMA1631	99
NMA1632	100
NMA1633	97
NMA1634	99
NMA1635	99
NMA1636	91
NMA1637	81
NMA1638	99
NMA1639	100
NMA1640	98
NMA1641	94
NMA1642	97
NMA1643	99
NMA1644	96
NMA1645	100
NMA1646	98
NMA1647	98

Figure 1 (cntd)

NMA1648	99
NMA1649	96
NMA1650	99
NMA1651	99
NMA1652	91
NMA1653	98
NMA1654	99
NMA1655	97
NMA1656	95
NMA1657	99
NMA1658	99
NMA1659	98
NMA1660	98
NMA1661	98
NMA1662	98
NMA1663	93
NMA1664	99
NMA1665	98
NMA1666	91
NMA1667	99
NMA1668	99
NMA1669	99
NMA1670	99
NMA1671	99
NMA1672	100
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NMA1674	99
NMA1675	98
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NMA1678	99
NMA1679	99
NMA1680	99
NMA1681	91
NMA1682	97
NMA1683	99
NMA1684	99
NMA1685	100
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NMA1688	100
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NMA1694	99
NMA1695	98
NMA1696	96
NMA1697	95
NMA1698	99
NMA1699	99
NMA1700	98
NMA1701	99
NMA1702	99
NMA1703	99

Figure 1 (cntd)

NMA1704	99
NMA1705	97
NMA1706	98
NMA1707	98
NMA1708	99
NMA1709	100
NMA1710	100
NMA1711	99
NMA1712	99
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NMA1719	99
NMA1720	99
NMA1721	97
NMA1722	100
NMA1723	93
NMA1724	97
NMA1725	90
NMA1726	100
NMA1727	98
NMA1728	95
NMA1729	93
NMA1730	98
NMA1731	100
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NMA1733	97
NMA1734	99
NMA1735	99
NMA1736	97
NMA1737	99
NMA1738	94
NMA1739	97
NMA1740	83
NMA1741	98
NMA1742	99
NMA1743	99
NMA1744	96
NMA1745	97
NMA1746	97
NMA1747	95
NMA1748	98
NMA1749	97
NMA1750	97
NMA1751	100
NMA1752	99
NMA1753	99
NMA1754	100
NMA1755	97
NMA1756	99
NMA1757	99
NMA1758	98
NMA1759	98

Figure 1 (cntd)

NMA1760	99
NMA1761	99
NMA1762	99
NMA1763	99
NMA1764	99
NMA1765	100
NMA1766	99
NMA1767	99
NMA1768	100
NMA1769	100
NMA1770	99
NMA1771	98
NMA1772	100
NMA1773	99
NMA1774	91
NMA1775	97
NMA1776	97
NMA1777	94
NMA1778	99
NMA1779	97
NMA1780	97
NMA1781	99
NMA1782	99
NMA1783	100
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NMA1785	99
NMA1786	99
NMA1788	97
NMA1792	99
NMA1793	98
NMA1794	99
NMA1795	95
NMA1796	100
NMA1797	93
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NMA1799	97
NMA1800	99
NMA1801	99
NMA1802	98
NMA1803	95
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NMA1808	98
NMA1809	95
NMA1810	98
NMA1811	98
NMA1812	99
NMA1813	99
NMA1814	99
NMA1815	98
NMA1816	98
NMA1817	99
NMA1818	98
NMA1819	98
NMA1820	100

Figure 1 (cntd)

NMA1828	67
NMA1851	66
NMA1852	93
NMA1854	84
NMA1858	100
NMA1859	100
NMA1860	98
NMA1861	95
NMA1862	97
NMA1863	99
NMA1864	96
NMA1866	77
NMA1868	80
NMA1883	73
NMA1884	84
NMA1886	98
NMA1887	98
NMA1888	91
NMA1890	84
NMA1891	100
NMA1892	100
NMA1894	99
NMA1895	100
NMA1896	99
NMA1897	98
NMA1898	93
NMA1899	97
NMA1900	98
NMA1901	99
NMA1902	99
NMA1903	98
NMA1904	99
NMA1905	99
NMA1906	98
NMA1907	99
NMA1907A	100
NMA1908	98
NMA1909	99
NMA1911	97
NMA1912	99
NMA1913	98
NMA1914	95
NMA1915	98
NMA1916	98
NMA1917	98
NMA1918	100
NMA1919	99
NMA1920	99
NMA1921	97
NMA1922	97
NMA1923	98
NMA1925	95
NMA1927	97
NMA1928	98
NMA1929	100
NMA1930	99

Figure 1 (cntd)

NMA1931	97
NMA1932	100
NMA1933	94
NMA1934	99
NMA1935	95
NMA1936	99
NMA1937	98
NMA1938	94
NMA1939	99
NMA1940	97
NMA1941	99
NMA1942	98
NMA1943	97
NMA1944	99
NMA1945	99
NMA1946	84
NMA1947	93
NMA1948	89
NMA1949	98
NMA1950	92
NMA1951	96
NMA1952	98
NMA1953	96
NMA1954	97
NMA1955	98
NMA1956	98
NMA1957	98
NMA1958	99
NMA1959	98
NMA1960	93
NMA1961	99
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NMA1965	98
NMA1966	97
NMA1967	97
NMA1968	98
NMA1969	99
NMA1970	97
NMA1971	99
NMA1972	98
NMA1973	99
NMA1974	96
NMA1975	97
NMA1976	98
NMA1977	99
NMA1978	100
NMA1979	99
NMA1980	100
NMA1981	98
NMA1982	99
NMA1983	100
NMA1984	100
NMA1985	99
NMA1986	99

Figure 1 (cntd)

NMA1987	99
NMA1988	100
NMA1989	99
NMA1990	100
NMA1991	96
NMA1992	92
NMA1994	99
NMA1995	95
NMA1996	95
NMA1997	99
NMA1998	99
NMA1999	98
NMA2000	96
NMA2001	100
NMA2002	99
NMA2003	100
NMA2004	99
NMA2005	100
NMA2006	100
NMA2007	100
NMA2008	100
NMA2009	100
NMA2010	99
NMA2011	96
NMA2012	97
NMA2013	98
NMA2014	99
NMA2015	99
NMA2016	100
NMA2017	99
NMA2018	97
NMA2019	98
NMA2020	99
NMA2021	97
NMA2022	100
NMA2023	99
NMA2024	97
NMA2025	82
NMA2026	100
NMA2027	99
NMA2028	97
NMA2030	97
NMA2031	100
NMA2032	98
NMA2033	97
NMA2034	97
NMA2035	99
NMA2036	98
NMA2037	98
NMA2038	97
NMA2039	98
NMA2040	99
NMA2041	98
NMA2043	81
NMA2044	96
NMA2045	99

Figure 1 (cntd)

NMA2046	99
NMA2047	98
NMA2048	99
NMA2049	99
NMA2050	99
NMA2051	99
NMA2052	98
NMA2053	99
NMA2054	100
NMA2055	99
NMA2056	99
NMA2057	100
NMA2058	99
NMA2059	99
NMA2060	98
NMA2061	99
NMA2062	98
NMA2063	99
NMA2064	96
NMA2065	69
NMA2066	99
NMA2067	96
NMA2068	98
NMA2069	94
NMA2071	98
NMA2072	100
NMA2073	100
NMA2074	98
NMA2075	98
NMA2076	98
NMA2077	98
NMA2078	97
NMA2079	96
NMA2080	98
NMA2081	98
NMA2083	100
NMA2084	93
NMA2085	97
NMA2086	96
NMA2087	91
NMA2088	93
NMA2089	99
NMA2090	98
NMA2091	99
NMA2092	97
NMA2093	96
NMA2094	96
NMA2097	96
NMA2098	97
NMA2099	99
NMA2100	99
NMA2101	99
NMA2102	99
NMA2103	97
NMA2105	98
NMA2106	99

Figure 1 (cntd)

NMA2107	100
NMA2108	99
NMA2109	100
NMA2111	99
NMA2112	98
NMA2113	69
NMA2114	85
NMA2115	69
NMA2117	99
NMA2118	95
NMA2120	97
NMA2122	99
NMA2123	98
NMA2124	99
NMA2126	98
NMA2127	98
NMA2128	98
NMA2129	98
NMA2130	99
NMA2131	98
NMA2132	100
NMA2133	99
NMA2134	96
NMA2135	98
NMA2136	96
NMA2137	97
NMA2138	96
NMA2139	97
NMA2140	96
NMA2141	98
NMA2142	100
NMA2143	97
NMA2144	99
NMA2145	100
NMA2146	97
NMA2147	100
NMA2148	98
NMA2149	98
NMA2150	99
NMA2151	98
NMA2152	99
NMA2153	99
NMA2154	96
NMA2155	100
NMA2156	93
NMA2157	99
NMA2158	98
NMA2159	100
NMA2160	99
NMA2161	100
NMA2162	100
NMA2163	100
NMA2164	98
NMA2165	100
NMA2166	100
NMA2167	99

Figure 1 (cntd)

NMA2168	99	
NMA2169	100	
NMA2170	98	
NMA2171	97	
NMA2172	99	Figure 1 (cntd)
NMA2173	96	
NMA2174	99	
NMA2175	96	
NMA2176	100	
NMA2177	99	
NMA2178	99	
NMA2179	99	
NMA2180	99	
NMA2181	83	
NMA2182	99	
NMA2183	96	
NMA2184	97	
NMA2185	97	
NMA2186	99	
NMA2187	98	
NMA2188	94	
NMA2189	98	
NMA2190	98	
NMA2191	100	
NMA2193	99	
NMA2195	99	
NMA2196	100	
NMA2197	98	
NMA2198	89	
NMA2199	96	
NMA2200	97	
NMA2201	99	
NMA2202	100	
NMA2203	99	
NMA2204	99	
NMA2205	98	
NMA2206	97	
NMA2207	98	
NMA2208	98	
NMA2209	99	
NMA2210	97	
NMA2211	96	
NMA2212	97	
NMA2213	98	
NMA2214	98	
NMA2215	97	
NMA2216	100	
NMA2217	98	
NMA2218	99	
NMA2219	96	
NMA2220	85	
NMA2221	98	
NMA2222	100	
NMA2223	98	
NMA2224	98	
NMA2225	96	

NMA2226	96
NMA2227	94
NMA2228	96
NMA2229	98

Figure 1 (cntd)

515 Genes mutated on 29/11/01

Figure 2A

The mutants in red present an increased sensitivity to the bactericidal action of the complement of human serum.

Nm2: *nuoL*, NADH dehydrogenase I chain L 8/1
 Nm3: unknown 35/25
 Nm10: *nuoG*, NADH dehydrogenase I chain G 16/33, 26/39
 Nm15: *nuoE*, NADH dehydrogenase I chain E 8/41
 Nm17: *nuoC*, NADH dehydrogenase I chain C 29/44, 57/25
 Nm18: *nuoB*, NADH dehydrogenase I chain B 7/39', 64/45'
 Nm20: probable integral membrane protein 20/44
 Nm22: possible transposase for IS1016 9/17
 Nm24: unknown 20/7
 Nm29: unknown 93/8
 Nm37: unknown 95/37
 Nm39: unknown 5/31, 24/16', 53/27', 93/13
 Nm42: *pyrD*, dihydroorotate dehydrogenase 79/39
 Nm47: probable transmembrane transport protein 71/19
 Nm48: *pglA*, glycosyltransferase 18/48
 Nm50: *katA*, catalase 60/22
 Nm60: probable transmembrane transport protein 4/37', 9/37, 80/37'
 Nm65: probable lipoprotein 19/44
 Nm67: unknown 49/30
 Nm70: *rluC*, probable ribosomal large subunit pseudouridine synthase C 1/44
 Nm73: probable amino-acid transport protein 14/46, 17/12
 Nm77: *gidB*, probable glucose inhibited division protein B homolog 20/24
 Nm83: *dxr*, probable 1-deoxy-D-xylulose-5-phosphate reductoisomerase 80/24
 Nm84: probable integral membrane protein 5/38

Nm155: unknown 7/37, 13/31', 25/45'
 Nm157: unknown 47/48
 Nm160: probable two-component sensor 92/36
 Nm162: SUN homolog 19/43
 Nm165: probable periplasmic protein 8/7, 8/15, 95/23
 Nm173: unknown 51/35
 Nm182: probable lipoprotein 9/42
 Nm183: *gltS*, sodium/glutamate symport carrier protein 72/40
 Nm184: unknown 19/1, 23/8, 57/10
 Nm185: *lipB*, capsule polysaccharide modification protein 19/14', 22/14', 25/9, 86/2
 Nm186: *lipA*, capsule polysaccharide modification protein 41/29, 80/4, 93/19
 Nm193: probable modification methylase 15/20, 25/6
 Nm195: *catA*, probable capsule polysaccharide export ATP-binding protein 17/5', 18/15', 93/47
 Nm198: *ctrA*, capsule polysaccharide export outer membrane protein 13/16, 43/8

Nm207: probable integral membrane protein 55/35
 Nm221: possible transposase for IS1106 12/5
 Nm225: possible lipoprotein 5/36, 15/9
 Nm228: unknown 28/25
 Nm229: unknown 93/38
 Nm233: probable lipoprotein 16/20
 Nm247: *mutS*, DNA mismatch repair protein 11/7, 11/16
 Nm251: probable periplasmic protein 1/21, 12/7', 12/17'', 12/19', 19/13'', 94/38
 Nm255: *ftsX*, probable ABC transporter integral membrane protein 16/5, 93/43
 Nm259: probable transmembrane transport protein 92/11
 Nm274: possible glycerate dehydrogenase 39/20', 47/12'
 Nm279: probable membrane-bound lytic murein transglycosylase 6/29, 70/13, 76/7, 95/47
 Nm285: probable lipoprotein 38/2
 Nm287: *thpA*, probable thiamin-binding periplasmic protein 1/38

515 genes mutated on 29/11/01

The underlined mutants present an increased sensitivity to the bactericidal action of the complement of human serum. The figures in bold identify each mutant by pool number/mutant number.

Nm2: *nuoL*, NADH dehydrogenase I chain L 8/1
 Nm3: unknown 35/25
 Nm10: *nuoG*, NADH dehydrogenase I chain G 16/33, 26/39
 Nm15: *nuoE*, NADH dehydrogenase I chain E 8/41
 Nm17: *nuoC*, NADH dehydrogenase I chain C 29/44, 57/25
 Nm18: *nuoB*, NADH dehydrogenase I chain B 7/39', 64/45'
 Nm20: probable integral membrane protein 20/44
 Nm22: possible transposase for IS1016 9/17
 Nm24: unknown 20/7
 Nm29: unknown 93/8
 Nm37: unknown 95/37
 Nm39: unknown 5/31, 24/16', 53/27', 93/13
 Nm42: *pyrD*, dihydroorotate dehydrogenase 79/39
 Nm47: probable transmembrane transport protein 71/19
 Nm48: *pglA*, glycosyltransferase 18/48
 Nm50: *katA*, catalase 60/22
 Nm60: probable transmembrane transport protein 4/37', 9/37, 80/37'
 Nm65: probable lipoprotein 19/44
 Nm67: unknown 49/30
 Nm70: *rluC*, probable ribosomal large subunit pseudouridine synthase C 1/44
 Nm73: probable amino-acid transport protein 14/46, 17/12
 Nm77: *gidB*, probable glucose inhibited division protein B homolog 20/24
Nm83: *dxr*, probable 1-deoxy-D-xylulose-5-phosphate reductoisomerase 80/24
 Nm84: probable integral membrane protein 5/38

Nm155: unknown 7/37, 13/31', 25/45'
 Nm157: unknown 47/48
 Nm160: probable two-component sensor 92/36
 Nm162: SUN homolog 19/43
 Nm165: probable periplasmic protein 8/7, 8/15, 95/23
 Nm173: unknown 51/35
 Nm182: probable lipoprotein 9/42
 Nm183: *gltS*, sodium/glutamate symport carrier protein 72/40
 Nm184: unknown 19/1, 23/8, 57/10
Nm185: *lipB*, capsule polysaccharide modification protein 19/14', 22/14', 25/9, 86/2
Nm186: *lipA*, capsule polysaccharide modification protein 41/29, 80/4, 93/19
 Nm193: probable modification methylase 15/20, 25/6
Nm195: *cwl*, probable capsule polysaccharide export ATP-binding protein 17/5', 18/15', 93/47
Nm198: *cfrA*, capsule polysaccharide export outer membrane protein 13/16, 43/8

Nm207: probable integral membrane protein 55/35
 Nm221: possible transposase for IS1106 12/5
 Nm225: possible lipoprotein 5/36, 15/9
 Nm228: unknown 28/25
Nm229: unknown 93/38
 Nm233: probable lipoprotein 16/20
 Nm247: *mutS*, DNA mismatch repair protein 11/7, 11/16
 Nm251: probable periplasmic protein 1/21, 12/7', 12/17'', 12/19', 19/13'', 94/38
 Nm255: *ftsX*, probable ABC transporter integral membrane protein 16/5, 93/43
 Nm259: probable transmembrane transport protein 92/11
 Nm274: possible glycerate dehydrogenase 39/20', 47/12'
 Nm279: probable membrane-bound lytic murein transglycosylase 6/29, 70/13, 76/7, 95/47
 Nm285: probable lipoprotein 38/2

Nm289: unknown 16/1
 Nm292: unknown 10/43
 Nm293: *pilC2*, pilus-associated protein 2/26, 94/28
 Nm298: probable symport protein 95/14

Figure 2A
 (cntd)

Nm307: unknown 12/28
 Nm319: *mafB'*, possible MafB alternative C-terminus 8/30
 Nm320: unknown 13/43
 Nm325: *mafA*, adhesin 5/25
 Nm348: putative nuclease 3/30, 20/4
 Nm349: probable integral membrane protein 46/7
 Nm353: probable integral membrane protein 22/45, 90/40
 Nm356: possible transferase 55/48
 Nm365: probable permease 4/33
 Nm368: probable integral membrane protein 12/36
 Nm369: *hemK*, HemK protein 81/39
 Nm370: probable integral membrane protein 46/43
 Nm372: unknown 7/18', 8/27'
 Nm374: *ppc*, phosphoenolpyruvate carboxylase 18/33, 18/38, 84/2
 Nm380: unknown 46/35
 Nm382: unknown 10/9
 Nm397: *thiC*, thiamin biosynthesis protein 13/33

Nm409: probable amino-acid transport protein 4/24
 Nm413: *gntP*, probable gluconate permease 10/47
 Nm414: probable permease 2/16, 5/46
 Nm422: probable pseudouridine synthase 6/9', 13/19, 20/15', 77/18
 Nm425: unknown 47/7
 Nm428: conserved hypothetical protein 3/31
 Nm433: *hrpA'*, ATP-dependent DNA helicase 44/4
 Nm434: hypothetical inner membrane protein 61/14
 Nm436: hypothetical inner membrane protein 93/32
 Nm441: conserved hypothetical protein 12/25
 Nm445: *purL*, phosphoribosylformylglycinamide synthase 4/17, 10/14', 11/8', 75/34
 Nm457: *iga2*, IgA-specific serine endopeptidase 9/21, 40/31
 Nm465: hypothetical inner membrane protein 71/2
 Nm478: possible outer membrane peptidase 6/43
 Nm481: unknown 27/21
 Nm485: probable ABC transport ATP-binding subunit 5/4, 16/45
 Nm486: possible ABC transport inner-membrane subunit 15/32
 Nm489: hypothetical protein 61/13
 Nm490: possible periplasmic/outer membrane protein 96/22
 Nm497: probable inner membrane protein 71/18
 Nm499: *regG*, possible regulator of *pilE* expression 7/44

Nm503: possible transglycosylase 6/19, 11/17, 16/17
 Nm506: possible lipoprotein 6/12
 Nm512: *atpI*, probable ATP synthase I 8/23
 Nm524: *lgtA*, lacto-N-neotetraose biosynthesis, glycosyl transferase 3/8, 10/2, 21/21, 45/34
 Nm531: pseudogene, probable transposase remnant 90/36
 Nm546: unknown 20/9
 Nm559: *leuS*, probable leucyl-tRNA synthetase 68/22
 Nm560: *drg*, probable type II restriction endonuclease 57/15
 Nm580: *argA*, probable acetylglutamate synthase 7/25
 Nm582: *pyrE*, probable orotate phosphoribosyltransferase 19/36, 57/31
 Nm587: *fba*, probable fructose-1,6-bisphosphate aldolase 21/25, 21/47
 Nm592: *hemL*, probable glutamate-1-semialdehyde 2,1-aminomutase 47/10
 Nm594: *orn*, probable oligoribonuclease 14/25
 Nm599: *queA*, probable S-adenosylmethionine-ribosyltransferase-isomerase 91/2, 96/23

Figure 2A
(cntd)

Nm287: *thpA*, probable thiamin-binding periplasmic protein 1/38
 Nm289: unknown 16/1
 Nm292: unknown 10/43
 Nm293: *pilC2*, pilus-associated protein 2/26, 94/28
 Nm298: probable symport protein 95/14

 Nm307: unknown 12/28
 Nm319: *mafB'*, possible MafB alternative C-terminus 8/30
 Nm320: unknown 13/43
 Nm325: *mafA*, adhesin 5/25
 Nm348: putative nuclease 3/30, 20/4
 Nm349: probable integral membrane protein 46/7
 Nm353: probable integral membrane protein 22/45, 90/40
 Nm356: possible transferase 55/48
 Nm365: probable permease 4/33
 Nm368: probable integral membrane protein 12/36
 Nm369: *hemK*, HemK protein 81/39
 Nm370: probable integral membrane protein 46/43
 Nm372: unknown 7/18', 8/27'
 Nm374: *ppc*, phosphoenolpyruvate carboxylase 18/33, 18/38, 84/2
 Nm380: unknown 46/35
 Nm382: unknown 10/9
 Nm397: *thiC*, thiamin biosynthesis protein 13/33

 Nm409: probable amino-acid transport protein 4/24
 Nm413: *gntP*, probable gluconate permease 10/47
 Nm414: probable permease 2/16, 5/46
 Nm422: probable pseudouridine synthase 6/9', 13/19, 20/15', 77/18
 Nm425: unknown 47/7
 Nm428: conserved hypothetical protein 3/31
 Nm433: *hrpA'*, ATP-dependent DNA helicase 44/4
 Nm434: hypothetical inner membrane protein 61/14
 Nm436: hypothetical inner membrane protein 93/32
 Nm441: conserved hypothetical protein 12/25
 Nm445: *purL*, phosphoribosylformylglycinamide synthase 4/17, 10/14', 11/8', 75/34
 Nm457: *iga2*, IgA-specific serine endopeptidase 9/21, 40/31
 Nm465: hypothetical inner membrane protein 71/2
 Nm478: possible outer membrane peptidase 6/43
 Nm481: unknown 27/21
 Nm485: probable ABC transport ATP-binding subunit 5/4, 16/45
 Nm486: possible ABC transport inner-membrane subunit 15/32
 Nm489: hypothetical protein 61/13
 Nm490: possible periplasmic/outer membrane protein 96/22
 Nm497: probable inner membrane protein 71/18
 Nm499: *regG*, possible regulator of *pilH* expression 7/44

 Nm503: possible transglycosylase 6/19, 11/17, 16/17
 Nm506: possible lipoprotein 6/12
 Nm512: *atpI*, probable ATP synthase 18/23
Nm524: *lgtA*, lacto-N-neotetraose biosynthesis glycosyl transferase 3/8, 10/2, 21/21, 45/34
 Nm531: pseudogene, probable transposase remnant 90/36
 Nm546: unknown 20/9
 Nm559: *leuS*, probable leucyl-tRNA synthetase 68/22
 Nm560: *drg*, probable type II restriction endonuclease 57/15
 Nm580: *argA*, probable acetylglutamate synthase 7/25
 Nm582: *pyrL*, probable orotate phosphoribosyltransferase 19/36, 57/31
 Nm587: *fbp*, probable fructose-1,6-bisphosphate aldolase 21/25, 21/47
 Nm592: *hemI*, probable glutamate-1-semialdehyde 2,1-aminomutase 47/10
 Nm594: *orn*, probable oligoribonuclease 14/25
 Nm599: *queA*, probable S-adenosylmethionine-ribosyltransferase-isomerase 91/2, 96/23

Figure 2A
(cntd)

Nm600: unknown 11/28
 Nm601: probable *lysR*-family transcriptional regulator 47/37
 Nm602: *carB*, carbamoyl phosphate synthase 2/13, 94/39
 Nm613: probable *marR*-family regulator 92/41
 Nm618: hypothetical protein 5/14, 91/41, 92/45
 Nm619: possible lipopolysaccharide modification acyltransferase 31/22, 46/36, 47/14, 96/11
 Nm629: unknown 9/6
 Nm630: unknown 10/4
 Nm631: unknown 6/46, 9/23, 15/22, 34/9
 Nm636: *avtA*, probable valine-pyruvate aminotransferase 7/22
 Nm638: *pglC*, pilin glycosylation protein 68/25
 Nm639: *pglB*, pilin glycosylation protein 90/45, 93/45
 Nm643: possible lipopolysaccharide biosynthesis translocase 43/13
 Nm646: unknown 7/16
 Nm650: *pilQ*, pilus secretin 10/33, 72/13
 Nm654: *pilM*, probable pilus assembly protein 11/33, 19/33
 Nm670: possible two-component system sensor kinase 1/14
 Nm672: unknown 69/23
 Nm679: unknown 1/43, 15/17
 Nm687: probable periplasmic protein 96/46
 Nm688: *fhaB*-like gene 3/24, 14/31, 16/2, 48/7, 87/6
 Nm690: unknown 10/21, 22/11
 Nm691: unknown, Asn-rich N-terminus 46/46
 Nm692: unknown 4/7, 20/27
 Nm693: unknown within a region of low G+C % 3/19
 Nm694: unknown within a region of low G+C % 7/17
 Nm696: unknown 1/40, 7/42

Nm714: probable transmembrane hexose transporter 2/14, 5/47
 Nm715: probable transmembrane transport protein 1/2, 6/45, 15/40
 Nm720: unknown 4/19, 14/7
 Nm722: probable transmembrane transport protein 41/25
 Nm725: *adhA*, probable alcohol dehydrogenase 7/20, 51/22
 Nm726: probable pilin (*acfP*) 11/24
 Nm729: probable ABC transporter ATP-binding protein 92/43
 Nm730: possible thiol-disulphide interchange protein 7/9, 10/18
 Nm740: unknown 6/10
 Nm741: possible ubiquinone biosynthesis protein 92/15
 Nm747: *nqrF*, probable Na⁺-translocating NADH-ubiquinone reductase subunit F 90/34
 Nm750: *nqrC*, probable Na⁺-translocating NADH-ubiquinone reductase subunit C 12/45
 Nm752: *nqrA*, probable Na⁺-translocating NADH-ubiquinone reductase subunit A 19/27, 96/39
 Nm753: possible membrane protein 7/46', 19/19, 28/21', 51/14, 95/45
 Nm755: unknown 70/11', 71/6', 73/5, 73/18
 Nm762: hypothetical protein 18/16, 90/29
 Nm786: possible membrane protein 78/23
 Nm796: unknown 92/2

Nm800: possible integral membrane protein 7/10, 29/28, 52/1, 69/14
 Nm801: unknown 6/5', 12/8'
 Nm802: unknown 30/25
 Nm804: possible sec-independent protein translocase component 93/25
 Nm816: probable polyamine permease ATP-binding protein 19/8
 Nm817: probable polyamine permease inner membrane protein 9/36
 Nm819: possible oxidoreductase 96/31
 Nm820: *amtB*, probable ammonium transporter 5/30
 Nm826: *pps4*, probable phosphoenolpyruvate synthase 8/47
 Nm827: unknown 7/11
 Nm828: probable phosphatase 36/3
 Nm832: possible glycosyl transferase 14/29, 48/26
 Nm843: *fbpB*, probable iron-uptake permease inner membrane protein 56/34

Nm600: unknown 11/28
 Nm601: probable *lysR*-family transcriptional regulator 47/37
 Nm602: *carB*, carbamoyl phosphate synthase 2/13, 94/39
 Nm613: probable *marR*-family regulator 92/41
 Nm618: hypothetical protein 5/14, 91/41, 92/45
 Nm619: possible lipopolysaccharide modification acyltransferase 31/22, 46/36, 47/14, 96/11
 Nm629: unknown 9/6
 Nm630: unknown 10/4
 Nm631: unknown 6/46, 9/23, 15/22, 34/9
 Nm636: *avtA*, probable valine-pyruvate aminotransferase 7/22
 Nm638: *pglC*, pilin glycosylation protein 68/25
 Nm639: *pglB*, pilin glycosylation protein 90/45, 93/45
 Nm643: possible lipopolysaccharide biosynthesis translocase 43/13
 Nm646: unknown 7/16
 Nm650: *pilQ*, pilus secretin 10/33, 72/13
 Nm654: *pilM*, probable pilus assembly protein 11/33, 19/33
 Nm670: possible two-component system sensor kinase 1/14
 Nm672: unknown 69/23
 Nm679: unknown 1/43, 15/17
 Nm687: probable periplasmic protein 96/46
 Nm688: *fhaB*-like gene 3/24, 14/31, 16/2, 48/7, 87/6
 Nm690: unknown 10/21, 22/11
 Nm691: unknown, Asn-rich N-terminus 46/46
 Nm692: unknown 4/7, 20/27
 Nm693: unknown within a region of low G+C % 3/19
 Nm694: unknown within a region of low G+C % 7/17
 Nm696: unknown 1/40, 7/42

 Nm714: probable transmembrane hexose transporter 2/14, 5/47
 Nm715: probable transmembrane transport protein 1/2, 6/45, 15/40
 Nm720: unknown 4/19, 14/7
 Nm722: probable transmembrane transport protein 41/25
 Nm725: *adhA*, probable alcohol dehydrogenase 7/20, 51/22
 Nm726: probable pilin (*acfP*) 11/24
 Nm729: probable ABC transporter ATP-binding protein 92/43
 Nm730: possible thiol-disulphide interchange protein 7/9, 10/18
 Nm740: unknown 6/10
 Nm741: possible ubiquinone biosynthesis protein 92/15
 Nm747: *nqrF*, probable Na⁺-translocating NADH-ubiquinone reductase subunit F 90/34
 Nm750: *nqrC*, probable Na⁺-translocating NADH-ubiquinone reductase subunit C 12/45
 Nm752: *nqrA*, probable Na⁺-translocating NADH-ubiquinone reductase subunit A 19/27, 96/39
 Nm753: possible membrane protein 7/46', 19/19, 28/21', 51/14, 95/45
 Nm755: unknown 70/11', 71/6', 73/5, 73/18
 Nm762: hypothetical protein 18/16, 90/29
 Nm786: possible membrane protein 78/23
 Nm796: unknown 92/2

 Nm800: possible integral membrane protein 7/10, 29/28, 52/1, 69/14
 Nm801: unknown 6/5', 12/8'
 Nm802: unknown 30/25
 Nm804: possible sec-independent protein translocase component 93/25
 Nm816: probable polyamine permease ATP-binding protein 19/8
 Nm817: probable polyamine permease inner membrane protein 9/36
 Nm819: possible oxidoreductase 96/31
 Nm820: *amtB*, probable ammonium transporter 5/30
 Nm826: *ppsA*, probable phosphoenolpyruvate synthase 8/47
 Nm827: unknown 7/11
 Nm828: probable phosphatase 36/3
 Nm832: possible glycosyl transferase 14/29, 48/26

Figure 2A
(cntd)

Nm845: unknown 6/8
 Nm847: *argH*, probable argininosuccinate lyase 95/5
 Nm848: *galU*, probable UTP-glucose-1-phosphate uridylyltransferase 32/37
 Nm867: *ampD*, probable anhydro-N-acetylmuramyl-tripeptide amidase 48/6
 Nm868: possible periplasmic protein 46/19
 Nm873: possible periplasmic protein 11/5
 Nm879: *trpA*, probable tryptophan synthase α chain 19/24, 65/48
 Nm884: *pyrC*, probable dihydroorotase 1/37, 89/9
 Nm888: *rnc*, probable ribonuclease III 6/47
 Nm890: *trpF*, probable N-(5'-phosphoribosyl)anthranilate isomerase 95/39
 Nm892: *purF*, probable amidophosphoribosyltransferase 60/4

Nm904: *trpB*, probable tryptophan synthase β chain 5/41, 8/40, 27/34', 85/25'
 Nm905: *iga*, IgA1 protease 1/39; 7/1, 9/25, 12/34
 Nm909: probable transmembrane transport protein 1/28, 9/22
 Nm915: unknown 3/37
 Nm928: *tgt*, probable queuine tRNA-ribosyltransferase 95/9
 Nm935: unknown 4/28, 75/44
 Nm941: unknown 2/45
 Nm942: *bioA*, probable adenosylmethionine-S-amino-7-oxononanoate aminotransferase 6/6, 33/2
 Nm944: unknown 7/13
 Nm948: unknown 32/26
 Nm952: *recN*, probable DNA repair protein 68/11
 Nm955: unknown 5/7
 Nm962: probable D-alanyl-D-alanine-endopeptidase 1/48, 56/18, 96/16
 Nm968: *purC*, probable phosphoribosylaminoimidazole-succinocarboxamide synthase 5/15
 Nm973: probable integral membrane protein 7/40, 44/34
 Nm977: *lepA*, probable GTP-binding protein 90/15
 Nm979: *pilT2*, possible pilus retraction protein 90/19
 Nm981: possible pilus biogenesis protein 11/22
 Nm982: unknown 1/24, 7/33
 Nm987: probable secreted protein 64/5
 Nm990: unknown 80/2
 Nm993: possible periplasmic protein 72/33
 Nm994: possible periplasmic protein 16/39
 Nm995: *recB*, probable exodeoxyribonuclease V β chain 8/42, 9/28, 41/35
 Nm999: probable amino acid permease integral membrane protein 73/39

Nm1001: *pgm*, phosphoglucomutase 2/46, 6/35, 25/5, 94/2
 Nm1002: *ppiB*, probable peptidyl-prolyl cis-trans isomerase B 94/18
 Nm1003: probable transmembrane transport protein 29/42
 Nm1008: *ftsJ*, probable cell division protein 15/1
 Nm1012: probable carbon-sulphur lyase 6/28, 92/4
 Nm1015: probable NAD(P)H-flavin oxidoreductase 25/14, 29/32
 Nm1016: probable RNA-binding protein 93/44
 Nm1020: probable *tetR*-family transcriptional regulator 28/41
 Nm1022: possible transmembrane efflux protein 8/22, 37/27
 Nm1034: *rfaE*, probable ADP-heptose synthetase 13/6
 Nm1035: *nmgII*, probable modification methylase 60/25, 93/11
 Nm1037: *rfaD*, probable ADP-L-glycero-mannoheptose epimerase 7/30, 47/39
 Nm1048: unknown 18/3, 35/37
 Nm1052: *recJ*, probable single-stranded-DNA-specific exonuclease 43/9
 Nm1054: possible periplasmic protein 6/2
 Nm1056: unknown 5/1
 Nm1062: *rdgC*, unknown 2/39
 Nm1073: unknown 11/13, 83/7
 Nm1074: possible membrane protein 10/16, 47/27
 Nm1084: possible periplasmic protein 15/26
 Nm1086: unknown 7/35
 Nm1087: possible transferase 4/29, 84/17
 Nm1090: possible periplasmic protein 7/27, 19/12
 Nm1107: possible membrane protein 96/8
 Nm1108: possible membrane protein 34/7
 Nm1110: probable pilin 12/39, 41/23
 Nm1111: unknown 18/19
 Nm1118: *kg*, CMP-N-acetylmuramyl- β -glucosaminide α -2,3-sulfoltransferase 9/46, 65/40, 73/46, 94/8
 Nm1126: probable transmembrane transport protein 46/38
 Nm1136: *metX*, probable homoserine O-acetyltransferase 3/11, 14/42
 Nm1138: *rpmE2*, possible additional 50S ribosomal protein 131 96/2
 Nm1139: *metF*, probable 5,10-methylenetetrahydrofolate reductase 92/29
 Nm1140: *metE*, probable 5-methyltetrahydropteroylglutamate-homocysteine methyltransferase 71/7

Figure 2A
(cntd)

- Nm843: *fhpB*, probable iron-uptake permease inner membrane protein 56/34
 Nm845: unknown 6/8
 Nm847: *argH*, probable argininosuccinate lyase 95/5
 Nm848: *galI*, probable UTP-glucose-1-phosphate uridylyltransferase 32/37
 Nm867: *ampD*, probable anhydro-N-acetylmuramyl-tripeptide amidase 48/6
 Nm868: possible periplasmic protein 46/19
 Nm873: possible periplasmic protein 11/5
 Nm879: *trpA*, probable tryptophan synthase α chain 19/24, 65/48
 Nm884: *pyrC*, probable dihydroorotase 1/37, 89/9
 Nm888: *rnc*, probable ribonuclease III 6/47
 Nm890: *trpF*, probable N-(5'-phosphoribosyl)anthranilate isomerase 95/39
 Nm892: *purF*, probable amidophosphoribosyltransferase 60/4

 Nm904: *trpB*, probable tryptophan synthase β chain 5/41, 8/40, 27/34', 85/25'
 Nm905: *iga*, IgA1 protease 1/39, 7/1, 9/25, 12/34
 Nm909: probable transmembrane transport protein 1/28, 9/22
 Nm915: unknown 3/37
 Nm928: *igt*, probable queuine tRNA-ribosyltransferase 95/9
 Nm935: unknown 4/28, 75/44
 Nm941: unknown 2/45
 Nm942: *bkuA*, probable adenosylmethionine-S-aminio-7-oxononanoate aminotransferase 6/6, 33/2
 Nm944: unknown 7/13
 Nm948: unknown 32/26
 Nm952: *recN*, probable DNA repair protein 68/11
 Nm955: unknown 5/7
 Nm962: probable D-alanyl-D-alanine-endopeptidase 1/48, 56/18, 96/16
 Nm968: *purC*, probable phosphoribosylaminoimidazole-succinocarboxamide synthase 5/15
 Nm973: probable integral membrane protein 7/40, 44/34
 Nm977: *lepA*, probable GTP-binding protein 90/15
 Nm979: *pilT*, possible pilus retraction protein 90/19
 Nm981: possible pilus biogenesis protein 11/22
 Nm982: unknown 1/24, 7/33
 Nm987: probable secreted protein 64/5
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 Nm994: possible periplasmic protein 16/39
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 Nm1035: *nmgH*, probable modification methylase 60/25, 93/11
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 Nm1056: unknown 5/1 Nm1062: *rdgC*, unknown 2/39
 Nm1073: unknown 11/13, 83/7 Nm1074: possible membrane protein 10/16, 47/27
 Nm1084: possible periplasmic protein 15/26
 Nm1086: unknown 7/35 Nm1087: possible transferase 4/29, 84/17
 Nm1090: possible periplasmic protein 7/27, 19/12
 Nm1107: possible membrane protein 96/8 Nm1108: possible membrane protein 34/7
 Nm1110: probable pilin 12/39, 41/23

Nm1143: *sdhC*, probable succinate dehydrogenase cytochrome B subunit 92/23
 succinate dehydrogenase flavoprotein subunit 4/39
 sulphur protein 18/44
 Nm1148: *gluA*, probable citrate synthase 16/6', 20/34', 81/36
 Nm1149: *sucA*, probable 2-oxoglutarate dehydrogenase E1 component 15/24
 Nm1152: possible membrane protein 13/7, 93/18, 95/6
 Nm1162: unknown 96/1
 Nm1163: *trpG*, probable anthranilate synthase component II 26/22', 48/1'
 Nm1164: *trpD*, probable anthranilate phosphoribosyltransferase 9/19
 Nm1174: unknown 11/45
 Nm1184: possible lipoprotein 11/25
 Nm1186: unknown 12/18
 Nm1195: unknown 6/33
 Nm1200: probable surface fibril protein 47/19', 52/12'
 Nm1206: probable oxidoreductase 6/48, 34/8, 77/17
 Nm1207: unknown 14/24
 Nm1228: unknown within a region of unusually low G+C % 23/29
 Nm1243: probable sulphate-binding protein 7/26
 Nm1248: possible periplasmic protein 5/37
 Nm1249: *abcZ*, probable ABC transporter ATP-binding protein 2/8, 78/6
 Nm1250: *dedA*, hypothetical protein 19/5
 Nm1254: *glyA*, probable serine hydroxymethyltransferase 42/20
 Nm1255: *ggt*, probable gamma-glutamyltranspeptidase 14/8, 92/27, 94/15
 Nm1263: unknown 89/16
 Nm1272: unknown 95/2
 Nm1276: possible membrane protein 5/43, 16/13, 20/40
 Nm1285: unknown 94/37
 Nm1286: possible phage transposase 82/19
 Nm1307: unknown 95/32
 Nm1313: unknown 18/13, 22/18, 94/35
 Nm1315: unknown 18/31, 93/10
 Nm1325: possible phage tail fibre protein 15/19
 Nm1331: ABC transporter ATP-binding protein 3/43, 22/25
 Nm1334: possible periplasmic protein 1/32, 43/17
 Nm1341: unknown 12/46
 Nm1348: unknown 76/13
 Nm1351: possible RNA methyltransferase 76/37
 Nm1356: *mpl*, possible UDP-N-acetylmuramate-L-alanyl-γ-D-glutamyl-meso-diaminopimelate ligase 11/38, 12/15
 Nm1362: *cysI*, probable sulphite reductase β subunit 25/23
 Nm1363: *cysJ*, probable sulphite reductase α subunit 4/38, 11/12
 Nm1365: *cysD*, probable sulphate adenylate transferase subunit 2 19/29
 Nm1366: *cysH*, probable phosphoadenosinephosphosulfate reductase 8/32
 Nm1367: *cysG*, sirohaem synthase 53/16
 Nm1369: unknown, similar to the C-terminal half of bacterial hypothetical proteins 8/34, 63/5
 Nm1371: *vacB*, probable ribonuclease 40/33
 Nm1372: *guaB*, probable inosine-5'-monophosphate dehydrogenase 65/17
 Nm1373: unknown 11/32, 27/42
 Nm1375: possible transcriptional regulator 95/8
 Nm1381: probable integral membrane protein 74/27
 Nm1385: probable type I restriction-modification system modification protein 93/14
 Nm1393: possible ABC transporter ATP-binding protein 11/31
 Nm1395: *hom*, probable homoserine dehydrogenase 16/37
 Nm1401: *recD*, exodeoxyribonuclease V α subunit 13/5', 14/39', 31/25
 Nm1408: unknown 12/31
 Nm1409: probable ABC-transporter ATP-binding protein 10/42, 18/21
 Nm1415: unknown 7/47
 Nm1417: possible molybdopterine-guanine dinucleotide biosynthesis protein A 10/20, 34/28
 Nm1418: probable two-component system sensor kinase 87/16
 Nm1421: *purM*, probable phosphoribosylformylglycinamide cyclo-ligase 7/5
 Nm1425: *ribA*, probable GTP cyclohydrolase II 91/3
 Nm1427: probable glycosyl transferase 42/9
 Nm1435: unknown within a region of low G+C % 19/6, 90/47
 Nm1438: possible integral membrane protein 15/6
 Nm1440: *thrC*, probable threonine synthase 87/24
 Nm1441: unknown 21/31
 Nm1445: unknown 9/15
 Nm1448: *radC*, probable DNA repair protein 3/36, 4/45
 Nm1450: *lenC*, probable 3-isopropylmalate dehydratase large subunit 68/2
 Nm1456: *lenB*, probable 3-isopropylmalate dehydrogenase 4/9, 40/35
 Nm1459: *aspA*, probable aspartate ammonia-lyase 19/34, 44/45, 52/9

Figure 2A
(cntd)

Nm1111: unknown 18/19
 Nm1118: *ky*, CMP-N-acetylneuraminate- β -galactosamido- α -2,3-sialyltransferase 9/46, 65/40, 73/46, 94/8
 Nm1126: probable transmembrane transport protein 46/38
 Nm1136: *metX*, probable homoserine O-acetyltransferase 3/11, 14/42
 Nm1138: *rpmE2*, possible additional 50S ribosomal protein L31 96/2
 Nm1139: *metF*, probable 5,10-methylenetetrahydrofolate reductase 92/29
 Nm1140: *metE*, probable 5-methyltetrahydropteroylglutamate-homocysteine methyltransferase 71/7
 Nm1143: *sdhC*, probable succinate dehydrogenase cytochrome B subunit 92/23
 Nm1145: *sdhA*, probable succinate dehydrogenase flavoprotein subunit 4/39
 Nm1146: *sdhB*, probable succinate dehydrogenase iron-sulphur protein 18/44
 Nm1148: *gltA*, probable citrate synthase 16/6', 20/34', 81/36
 Nm1149: *sucA*, probable 2-oxoglutarate dehydrogenase E1 component 15/24
 Nm1152: possible membrane protein 13/7, 93/18, 95/6
 Nm1162: unknown 96/1
 Nm1163: *trpG*, probable anthranilate synthase component II 26/22', 48/1'
 Nm1164: *trpD*, probable anthranilate phosphoribosyltransferase 9/19
 Nm1174: unknown 11/45
 Nm1184: possible lipoprotein 11/25
 Nm1186: unknown 12/18
 Nm1195: unknown 6/33

 Nm1200: probable surface fibril protein 47/19', 52/12'
 Nm1206: probable oxidoreductase 6/48, 34/8, 77/17
 Nm1207: unknown 14/24
 Nm1228: unknown within a region of unusually low G+C % 23/29
 Nm1243: probable sulphate-binding protein 7/26
 Nm1248: possible periplasmic protein 5/37
 Nm1249: *abcZ*, probable ABC transporter ATP-binding protein 2/8, 78/6
 Nm1250: *dedA*, hypothetical protein 19/5
 Nm1254: *glyA*, probable serine hydroxymethyltransferase 42/20
 Nm1255: *ggT*, probable gamma-glutamyltranspeptidase 14/8, 92/27, 94/15
 Nm1263: unknown 89/16
 Nm1272: unknown 95/2
 Nm1276: possible membrane protein 5/43, 16/13, 20/4
 Nm1285: unknown 94/37
 Nm1286: possible phage transposase 82/19

 Nm1307: unknown 95/32
 Nm1313: unknown 18/13, 22/18, 94/35
 Nm1315: unknown 18/31, 93/10
 Nm1325: possible phage tail fibre protein 15/19
 Nm1331: ABC transporter ATP-binding protein 3/43, 22/25
 Nm1334: possible periplasmic protein 1/32, 43/17
 Nm1341: unknown 12/46
 Nm1348: unknown 76/13
 Nm1351: possible RNA methyltransferase 76/37
 Nm1356: *npf*, possible UDP-N-acetylneuramite-1- α -aryl- γ -D-glutaryl-meso-diaminopimelate lyase 11/38, 12/15
 Nm1362: *cysI*, probable sulphite reductase β subunit 25/23
 Nm1363: *cysJ*, probable sulphite reductase α subunit 4/38, 11/12
 Nm1365: *cysJ*, probable sulphate adenylate transferase subunit 2 19/29
 Nm1366: *cysH*, probable phosphoadenosinephosphosulfate reductase 8/32
 Nm1367: *cysI*, sirohaem synthase 53/16
 Nm1369: unknown, similar to the C-terminal half of bacterial hypothetical proteins 8/34, 63/5
 Nm1371: *vacB*, probable ribonuclease 40/33
 Nm1372: *guaB*, probable inosine-5'-monophosphate dehydrogenase 65/17
 Nm1373: unknown 11/32, 27/42
 Nm1375: possible transcriptional regulator 95/8
 Nm1381: probable integral membrane protein 74/27
 Nm1385: probable type I restriction-modification system modification protein 93/14
 Nm1393: possible ABC transporter ATP-binding protein 11/31
 Nm1395: *hom*, probable homoserine dehydrogenase 16/37

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Nm1460: probable integral membrane protein 11/27
 Nm1461: probable *dnaJ*-family protein 5/35
 Nm1465: unknown 95/25
 Nm1466: probable type III restriction-modification system endonuclease protein 8/43
 Nm1467: type III restriction-modification system 4/25
 Nm1473: unknown 15/35
 Nm1475: unknown 7/31, 8/8', 8/18', 92/5'', 92/12'', 92/44
 Nm1482: probable acyl-CoA ligase 5/39
 Nm1483: probable transmembrane transport protein 10/34, 14/11
 Nm1485: *gcr*, site-specific recombinase 13/39, 15/48
 Nm1491: *mfd*, transcription-repair coupling factor 14/3

Nm1500: probable modification methylase 19/37', 36/37'
 Nm1507: possible membrane-bound lytic murcin transglycosylase 5/28, 86/5, 90/27
 Nm1508: possible ribosomal small subunit pseudouridine synthase 19/21, 56/44
 Nm1509: possible sodium-dependent transporter 25/25
 Nm1518: *adhC*, alcohol dehydrogenase class III, glutathione-dependent formaldehyde dehydrogenase 18/25, 34/26, 94/48
 Nm1519: *esd*, esterase D 13/44
 Nm1523: possible lipoprotein 19/4
 Nm1528: *uraA*, uracil permease 10/22, 40/6
 Nm1533: conserved hypothetical integral membrane protein 7/14
 Nm1540: *uvrC*, excinuclease ABC subunit C 63/12
 Nm1541: unknown 3/5
 Nm1542: conserved hypothetical protein 96/42
 Nm1545: *uvrB*, excinuclease ABC subunit B 43/4
 Nm1547: possible secreted lysine-rich protein 8/3
 Nm1557: unknown 11/11
 Nm1558: possible TonB-dependent receptor protein 1/31
 Nm1565: probable aldehyde dehydrogenase 2/36
 Nm1571: iron/sulphur-binding oxidoreductase 90/18
 Nm1574: possible integral membrane transporter 11/35, 46/17, 74/48
 Nm1575: *xseA*, exonuclease VII large subunit 6/23
 Nm1577: unknown 12/6
 Nm1579: unknown 19/48, 66/14
 Nm1580: probable ATP-dependent RNA helicase 53/9
 Nm1584: *argD*, acetylmethionine aminotransferase 9/48
 Nm1589: conserved hypothetical protein 45/18
 Nm1590: probable type III restriction/modification system modification methylase 15/5
 Nm1592: *lldA*, L-lactate dehydrogenase 8/4', 20/1', 77/12

Nm1603: unknown 96/13
 Nm1617: *sodC*, superoxide dismutase 1/47
 Nm1639: probable integral membrane protein 61/48
 Nm1642: *porA*, porin, class I outer membrane protein 6/4
 Nm1645: possible lipoprotein 92/13
 Nm1646: phospholipase D-family protein 8/36, 14/4, 40/22, 95/48
 Nm1647: probable integral membrane protein 4/14, 10/3, 27/35
 Nm1660: *rep*, ATP-dependent DNA helicase 22/2
 Nm1665: possible DNA polymerase III subunit 3/48, 9/27
 Nm1679: *ppX/pppA*, possible exophosphatase 4/44
 Nm1687: probable glutamate dehydrogenase 15/36
 Nm1689: possible regulatory protein 9/9
 Nm1690: unknown 11/4

Nm1702: *rhh*, ribonuclease 6/34', 8/39'
 Nm1709: binding-protein-dependent transport systems inner membrane protein 3/28, 8/9
 Nm1715: possible integral membrane protein 11/20
 Nm1720: unknown 8/26
 Nm1722: possible cis-trans isomerase 3/47
 Nm1723: possible proline-rich repeat protein 96/24

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Nm1401: *recD*, exodeoxyribonuclease V α subunit 13/5', 14/39', 31/25
 Nm1408: unknown 12/31
 Nm1409: probable ABC-transporter ATP-binding protein 10/42, 18/21
 Nm1415: unknown 7/47
 Nm1417: possible molybdopterin-guanine dinucleotide biosynthesis protein A 10/20, 34/28
 Nm1418: probable two-component system sensor kinase 87/16
 Nm1421: *purM*, probable phosphoribosylformylglycinamide cyclo-ligase 7/5
 Nm1425: *ribA*, probable GTP cyclohydrolase II 91/3
 Nm1427: probable glycosyl transferase 42/9
 Nm1435: unknown within a region of low G+C % 19/6, 90/47
 Nm1438: possible integral membrane protein 15/6
 Nm1440: *thrC*, probable threonine synthase 87/24
 Nm1441: unknown 21/31
 Nm1445: unknown 9/15
 Nm1448: *radC*, probable DNA repair protein 3/36, 4/45
 Nm1450: *leuC*, probable 3-isopropylmalate dehydratase large subunit 68/2
 Nm1456: *leuB*, probable 3-isopropylmalate dehydrogenase 4/9, 40/35
 Nm1459: *aspA*, probable aspartate ammonia-lyase 19/34, 44/45, 52/9
 Nm1460: probable integral membrane protein 11/27
 Nm1461: probable *dnaJ*-family protein 5/35
 Nm1465: unknown 95/25
 Nm1466: probable type III restriction-modification system endonuclease protein 8/43
 Nm1467: type III restriction-modification system 4/25
 Nm1473: unknown 15/35
 Nm1475: unknown 7/31, 8/8', 8/18', 92/5'', 92/12'', 92/44
 Nm1482: probable acyl-CoA ligase 5/39
 Nm1483: probable transmembrane transport protein 10/34, 14/11
 Nm1485: *gcr*, site-specific recombinase 13/39, 15/48
 Nm1491: *mfd*, transcription-repair coupling factor 14/3

 Nm1500: probable modification methylase 19/37', 36/37'
 Nm1507: possible membrane-bound lytic murein transglycosylase 5/28, 86/5, 90/27
 Nm1508: possible ribosomal small subunit pseudouridine synthase 19/21, 56/44
 Nm1509: possible sodium-dependent transporter 25/25
 Nm1518: *adhC*, alcohol dehydrogenase class III, glutathione-dependent formaldehyde dehydrogenase 18/25, 34/26, 94/48
 Nm1519: *esd*, esterase D 13/44
 Nm1523: possible lipoprotein 19/4
 Nm1528: *uraA*, uracil permease 10/22, 40/6
 Nm1533: conserved hypothetical integral membrane protein 7/14
 Nm1540: *uvrC*, excinuclease ABC subunit C 63/12
 Nm1541: unknown 3/5
 Nm1542: conserved hypothetical protein 96/42
 Nm1545: *uvrB*, excinuclease ABC subunit B 43/4
 Nm1547: possible secreted lysine-rich protein 8/3
 Nm1557: unknown 11/11
 Nm1558: possible TonB-dependent receptor protein 1/31
 Nm1565: probable aldehyde dehydrogenase 2/36
 Nm1571: iron/sulphur-binding oxidoreductase 90/18
 Nm1574: possible integral membrane transporter 11/35, 46/17, 74/48
 Nm1575: *xseA*, exonuclease VII large subunit 6/23
 Nm1577: unknown 12/6
 Nm1579: unknown 19/48, 66/14
 Nm1580: probable ATP-dependent RNA helicase 53/9
 Nm1584: *argD*, acetylornithine aminotransferase 9/48
 Nm1589: conserved hypothetical protein 45/18
 Nm1590: probable type III restriction/modification system modification methylase 15/5
 Nm1592: *lldA*, L-lactate dehydrogenase 8/4', 20/1', 77/12

 Nm1603: unknown 96/13

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Nm1727: *rfaF*, ADP-heptose:LPS heptosyltransferase II 70/7
 Nm1731: conserved hypothetical protein 94/27
 Nm1740: *lbpB*, lactoferrin-binding protein 37/17
 Nm1751: possible *gntR*-family transcriptional regulator 90/30
 Nm1754: unknown 14/35
 Nm1755: *purN*, phosphoribosylglycinamide transformylase 2/2
 Nm1756: possible peptidyl-prolyl isomerase 1/42, 15/10
 Nm1765: *ilvH*, acetolactate synthase isozyme III small subunit 52/29
 Nm1767: possible lipoprotein 96/34
 Nm1771: *hisC*, histidinol-phosphate aminotransferase 19/39
 Nm1775: partial ORF 93/46
 Nm1778: possible secreted protease 35/1
 Nm1783: AraC-family transcriptional regulator 51/3
 Nm1785: conserved hypothetical integral membrane protein 96/15
 Nm1786: possible polyamine permease substrate-binding protein 29/6, 96/5

Nm1812: *fumA*, fumarate hydratase 2/15, 4/41
 Nm1816: conserved, possible DNA-binding, hypothetical protein 93/12
 Nm1819: conserved hypothetical protein 12/35, 92/21
 Nm1820: *gpxA*, glutathione peroxidase 1/13
 Nm1886: *nor*, nitric oxide reductase 4/30, 8/38, 10/7, 12/43, 13/20, 67/32, 80/16
 Nm1887: *aniA*, nitrite reductase 17/6
 Nm1892: conserved hypothetical protein 2/27
 Nm1894: *serC*, phosphoserine aminotransferase 36/4

Nm1900: possible haemolysin 8/12
 Nm1901: possible sodium-alanine symporter 2/9, 22/5
 Nm1920: *apt*, adenine phosphoribosyltransferase 9/35, 13/35, 34/1, 49/6
 Nm1921: conserved hypothetical protein 58/4, 86/44
 Nm1925: *hmbR*, haemoglobin receptor 11/19, 25/40, 62/9
 Nm1928: hypothetical integral membrane protein 93/33
 Nm1929: hypothetical integral membrane protein 9/40
 Nm1934: *gcvP*, glycine dehydrogenase 4/23, 18/39, 21/35, 32/27, 47/4
 Nm1935: unknown 59/44, 95/10
 Nm1936: probable cytochrome 71/35
 Nm1937: *tyrB*, aromatic amino acid aminotransferase 2/30, 20/19, 47/36, 57/6, 63/23
 Nm1938: *trmA*, tRNA (uracil-5-)-methyltransferase 16/21
 Nm1939: *aroC*, chorismate synthase 88/14
 Nm1940: unknown 23/31, 94/19
 Nm1944: *ldhA*, D-lactate dehydrogenase 60/10
 Nm1946: conserved hypothetical protein 18/28
 Nm1951: unknown 4/6, 37/39
 Nm1953: unknown 80/23
 Nm1957: *fubF2*, 3-oxoacyl-(acyl-carrier-protein) synthase II 11/44, 17/8
 Nm1958: *lgtF*, β -1,4-glucosyltransferase 3/15', 23/19', 57/11'', 71/8'', 71/10''
 Nm1960: unknown 2/11
 Nm1961: probable integral membrane ion transporter 10/12
 Nm1969: *mtrD*, probable drug efflux protein 36/36
 Nm1970: *mtrC*, membrane fusion protein 76/30, 92/42
 Nm1973: hypothetical integral membrane protein 2/40, 12/2
 Nm1975: possible integral membrane protein 27/20, 94/9
 Nm1983: *exbD*, biopolymer transport protein 85/3
 Nm1984: *exbB*, biopolymer transport protein 37/33
 Nm1996: *natD*, possible periplasmic type I secretion system protein, N-terminal region 6/42

Nm2007: unknown 12/24
 Nm2009: unknown 3/10
 Nm2010: hypothetical protein 5/10, 49/17
 Nm2011: conserved hypothetical protein 94/36, 95/36
 Nm2012: conserved hypothetical protein 43/12

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Nm1617: *sodC*, superoxide dismutase 1/47
 Nm1639: probable integral membrane protein 61/48
 Nm1642: *porA*, porin, class I outer membrane protein 6/4
 Nm1645: possible lipoprotein 92/13
 Nm1646: phospholipase D-family protein 8/36, 14/4, 40/22, 95/48
 Nm1647: probable integral membrane protein 4/14, 10/3, 27/35
 Nm1660: *rep*, ATP-dependent DNA helicase 22/2
 Nm1665: possible DNA polymerase III subunit 3/48, 9/27
 Nm1679: *ppX/gppA*, possible exophosphatase 4/44
 Nm1687: probable glutamate dehydrogenase 15/36
 Nm1689: possible regulatory protein 9/9
 Nm1690: unknown 11/4

 Nm1702: *rbh*, ribonuclease 6/34', 8/39'
 Nm1709: binding-protein-dependent transport systems inner membrane protein 3/28, 8/9
 Nm1715: possible integral membrane protein 11/20
 Nm1720: unknown 8/26
 Nm1722: possible cis-trans isomerase 3/47
 Nm1723: possible proline-rich repeat protein 96/24
 Nm1727: *rfaF*, ADP-heptose:LPS heptosyltransferase II 70/7
 Nm1731: conserved hypothetical protein 94/27
 Nm1740: *lbpB*, lactoferrin-binding protein 37/17
 Nm1751: possible *gntR*-family transcriptional regulator 90/30
 Nm1754: unknown 14/35
 Nm1755: *purN*, phosphoribosylglycinamide transformylase 2/2
 Nm1756: possible peptidyl-prolyl isomerase 1/42, 15/10
 Nm1765: *ilvH*, acetolactate synthase isozyme III small subunit 52/29
 Nm1767: possible lipoprotein 96/34
 Nm1771: *hisC*, histidinol-phosphate aminotransferase 19/39
 Nm1775: partial ORF 93/46
 Nm1778: possible secreted protease 35/1
 Nm1783: AraC-family transcriptional regulator 51/3
 Nm1785: conserved hypothetical integral membrane protein 96/15
 Nm1786: possible polyamine permease substrate-binding protein 29/6, 96/5

 Nm1812: *fumA*, fumarate hydratase 2/15, 4/41
 Nm1816: conserved, possible DNA-binding, hypothetical protein 93/12
 Nm1819: conserved hypothetical protein 12/35, 92/21
 Nm1820: *gpxA*, glutathione peroxidase 1/13
 Nm1886: *nor*, nitric oxide reductase 4/30, 8/38, 10/7, 12/43, 13/20, 67/32, 80/16
 Nm1887: *aniA*, nitrite reductase 17/6
 Nm1892: conserved hypothetical protein 2/27
 Nm1894: *serC*, phosphoserine aminotransferase 36/4

 Nm1900: possible haemolysin 8/12
 Nm1901: possible sodium-alanine symporter 2/9, 22/5
 Nm1920: *apt*, adenine phosphoribosyltransferase 9/35, 13/35, 34/1, 49/6
 Nm1921: conserved hypothetical protein 58/4, 86/44
 Nm1925: *hmbR*, haemoglobin receptor 11/19, 25/40, 62/9
 Nm1928: hypothetical integral membrane protein 93/33
 Nm1929: hypothetical integral membrane protein 9/40
 Nm1934: *gevP*, glycine dehydrogenase 4/23, 18/39, 21/35, 32/27, 47/4
 Nm1935: unknown 59/44, 95/10
 Nm1936: probable cytochrome 71/35
 Nm1937: *tyrB*, aromatic amino acid aminotransferase 2/30, 20/19, 47/36, 57/6, 63/23
 Nm1938: *trmA*, tRNA (uracil-5-)-methyltransferase 16/21
 Nm1939: *uroC*, chorismate synthase 88/14
 Nm1940: unknown 23/31, 94/19
 Nm1944: *ldhA*, D-lactate dehydrogenase 60/10
 Nm1946: conserved hypothetical protein 18/28

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Nm2016: *speB*, agmatinase 1/46', 42/46'
 Nm2020: possible integral membrane protein 92/18
 Nm2021: possible phospholipase 3/38
 Nm2028: *amiC*, N-acetylmuramoyl-L-alanine amidase 78/47
 Nm2029: unknown 7/21
 Nm2036: unknown within a region of low G+C % 56/23
 Nm2038: *recO*, DNA repair protein 16/44
 Nm2040: possible integral membrane efflux protein 95/33
 Nm2046: hypothetical integral membrane protein 11/18
 Nm2048: conserved hypothetical protein 41/12, 81/22
 Nm2052: *acnA*, aconitate hydratase 38/25
 Nm2054: *prpC*, citrate synthase 2 8/28, 91/29, 96/30
 Nm2069: probable integral membrane protein 3/4, 31/5
 Nm2076: conserved hypothetical protein 13/2
 Nm2078: possible thiol-disulphide interchange protein 2/31, 24/13
 Nm2083: *putP*, sodium/proline symporter 30/33
 Nm2084: *putA*, bifunctional PutA protein 13/42, 16/10
 Nm2086: *xthA*, exodeoxyribonuclease III 86/31
 Nm2092: *nadB*, L-aspartate oxidase 2/4, 47/24
 Nm2098: *mapA*, possible maltose phosphorylase 5/34
 Nm2099: *galM*, aldose 1-epimerase (mutarotase) 11/10

Nm2100: possible maltose/H⁺ symporter 9/38, 70/40
 Nm2101: ABC transporter ATP-binding protein 1/19', 5/18', 14/4, 38/23, 90/44
 Nm2113: *mafB2*, adhesin 2/7, 4/42, 10/32, 38/24
 Nm2118: hypothetical protein within a region of low G+C % 12/32, 24/11, 68/23
 Nm2120: hypothetical protein within a region of low G+C % 3/23, 78/24
 Nm2122: hypothetical protein within a region of low G+C % 20/13, 29/3
 Nm2123: *frpC'*, possible partial CDS 16/30
 Nm2124: possible outer membrane protein 43/5
 Nm2129: *aroE*, shikimate dehydrogenase 49/7
 Nm2130: *mtgA*, monofunctional biosynthetic peptidoglycan transglycosylase 52/6
 Nm2131: possible ABC transporter ATP-binding protein 13/10
 Nm2136: *tai*, transaldolase 92/9
 Nm2137: hypothetical protein within a region of low G+C % 11/14', 11/42', 96/47
 Nm2140: conserved hypothetical protein 1/11, 4/13, 66/4
 Nm2142: possible periplasmic hypothetical protein 46/40
 Nm2145: possible morphogene 19/45, 23/18, 32/22, 75/47
 Nm2146: *tspA*, *Neisseria*-specific antigen protein 9/9
 Nm2151: *ilvE*, probable branched-chain amino acid aminotransferase 41/31, 66/34
 Nm2155: *pilG*, pilus-assembly protein 2/19, 14/45, 25/19, 67/33, 85/28
 Nm2156: *pilD*, prepilin leader peptidase 4/16
 Nm2158: conserved hypothetical protein 1/10
 Nm2159: *pilF*, type IV pilus assembly protein 73/27
 Nm2167: hypothetical protein 1/12
 Nm2168: *emrB*, multidrug resistance translocase 33/39, 57/48
 Nm2171: conserved hypothetical inner membrane protein 4/35, 6/20
 Nm2172: conserved hypothetical protein, possible peptidase 6/38
 Nm2174: conserved hypothetical protein 6/41
 Nm2175: *vapA*, possible virulence associated protein 29/25
 Nm2178: conserved hypothetical protein 2/48
 Nm2180: *uroG*, phospho-2-dehydro-3-deoxyheptonate aldolase 78/10
 Nm2183: *opcB*, outer membrane protein 32/30
 Nm2186: hypothetical protein 19/22
 Nm2189: hypothetical inner membrane protein 2/6', 2/10'
 Nm2193: possible TonB-dependent receptor protein 71/23

Nm2200: *dinG*, probable ATP-dependent DNA helicase 83/44
 Nm2204: hypothetical protein 1/23, 3/12
 Nm2212: *trpC'*, indole-3-glycerol phosphate synthase 83/13

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Nm1951: unknown 4/6, 37/39
 Nm1953: unknown 80/23
 Nm1957: *fabF2*, 3-oxoacyl-(acyl-carrier-protein) synthase II 11/44, 17/8
 Nm1958: *lgtI'*, β -1,4-glucosyltransferase 3/15', 23/19', 57/11'', 71/8'', 71/10''
 Nm1960: unknown 2/11
 Nm1961: probable integral membrane ion transporter 10/12
 Nm1969: *mtrD*, probable drug efflux protein 36/36
 Nm1970: *mtrC*, membrane fusion protein 76/30, 92/42
 Nm1973: hypothetical integral membrane protein 2/40, 12/2
 Nm1975: possible integral membrane protein 27/20, 94/9
 Nm1983: *exbD*, biopolymer transport protein 85/3
 Nm1984: *exbB*, biopolymer transport protein 37/33
 Nm1996: *natD'*, possible periplasmic type I secretion system protein, N-terminal region 6/42

 Nm2007: unknown 12/24
 Nm2009: unknown 3/10
 Nm2010: hypothetical protein 5/10, 49/17
 Nm2011: conserved hypothetical protein 94/36, 95/36
 Nm2012: conserved hypothetical protein 43/12
 Nm2016: *speB*, agmatinase 1/46', 42/46'
 Nm2020: possible integral membrane protein 92/18
 Nm2021: possible phospholipase 3/38
 Nm2028: *amiC*, N-acetylmuramoyl-L-alanine amidase 78/47
 Nm2029: unknown 7/21
 Nm2036: unknown within a region of low G+C % 56/23
 Nm2038: *recO*, DNA repair protein 16/44
 Nm2040: possible integral membrane efflux protein 95/33
 Nm2046: hypothetical integral membrane protein 11/18
 Nm2048: conserved hypothetical protein 41/12, 81/22
 Nm2052: *acnA*, aconitate hydratase 38/25
 Nm2054: *prpC*, citrate synthase 2 8/28, 91/29, 96/30
 Nm2069: probable integral membrane protein 3/4, 31/5
 Nm2076: conserved hypothetical protein 13/2
 Nm2078: possible thiol-disulphide interchange protein 2/31, 24/13
 Nm2083: *putP*, sodium/proline symporter 30/33
 Nm2084: *putA*, bifunctional PutA protein 13/42, 16/10
 Nm2086: *xthA*, exodeoxyribonuclease III 86/31
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 Nm2098: *mapA*, possible maltose phosphorylase 5/34
 Nm2099: *galM*, aldose 1-epimerase (mutarotase) 11/10

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 Nm2101: ABC transporter ATP-binding protein 1/19', 5/18', 14/4, 38/23, 90/44
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 Nm2118: hypothetical protein within a region of low G+C % 12/32, 24/11, 68/23
 Nm2120: hypothetical protein within a region of low G+C % 3/23, 78/24
 Nm2122: hypothetical protein within a region of low G+C % 20/13, 29/3
 Nm2123: *frpC''*, possible partial CDS 16/30
 Nm2124: possible outer membrane protein 43/5
 Nm2129: *arolE*, shikimate dehydrogenase 49/7
 Nm2130: *migA*, monofunctional biosynthetic peptidoglycan transglycosylase 52/6
 Nm2131: possible ABC transporter ATP-binding protein 13/10
 Nm2136: *tal*, transaldolase 92/9
 Nm2137: hypothetical protein within a region of low G+C % 11/14', 11/42', 96/47
 Nm2140: conserved hypothetical protein 1/11, 4/13, 66/4
 Nm2142: possible periplasmic hypothetical protein 46/40
 Nm2145: possible morphogene 19/45, 23/18, 32/22, 75/47
 Nm2146: *tspA*, *Neisseria*-specific antigen protein 9/9
 Nm2151: *thyE*, probable branched-chain amino acid aminotransferase 41/31, 66/34
 Nm2155: *pilG*, pilus-assembly protein 2/19, 14/45, 25/19, 67/33, 85/28

Nm2216: possible hydrolase 75/11
 Nm2218: possible tRNA/rRNA methyltransferase 1/15
 Nm2223: probable ABC transporter 16/9
 Nm2225: *xseB*, exodeoxyribonuclease small subunit 42/37

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Nm188 or Nm205: *rfbA*, glucose-1-phosphate thymidyltransferase 27/38', 35/36', 35/39', 37/2', 58/8
 Nm293 or Nm609: *pilC2* or *pilC1*, pilus-associated protein 5/42
 Nm525 or Nm527: *lgtB*, lacto-N-neotetraose biosynthesis glycosyl transferase 3/39
 Nm690 or Nm692: unknown 91/33
 Nm788 or Nm1626: *fpa* or *f7C*, exotoxin 3/17, 4/36', 7/36', 9/1, 13/41, 18/36, 19/7, 21/17'', 24/17'', 27/28, 65/27, 67/22
 Nm1167 or Nm1999: possible phage protein 12/37, 18/37
 Nm1169 or Nm2001: unknown 78/44
 Nm1196 or Nm1310: unknown 8/44
 Nm1186 or Nm1301: unknown 49/23, 56/37
 Nm1313 or Nm1852: unknown 20/16
 Nm1780 or Nm1781: doubtful ORFs 94/44

NmB65: hypothetical protein 61/44, 77/4
 NmB69: *siaB*, polysialic acid capsule biosynthesis protein 28/22
 NmB70: *synX*, polysialic acid capsule biosynthesis protein 77/19
 NmB91: hypothetical protein 1/4
 NmB98: ABC transporter, ATP-binding protein 7/23, 65/6, 69/1
 NmB223: hypothetical protein 30/6
 NmB372: hypothetical protein 84/20
 NmB493: hemagglutinin/hemolysin-related protein 11/1, 12/1
 NmB648: hypothetical protein 5/40
 NmB653: MafB-related protein 12/21
 NmB896: integrase 16/22, 43/15, 94/14
 NmB1502: hypothetical protein 4/3, 76/31
 NmB1603 tellurite resistance protein 28/10
 NmB1759: conserved hypothetical protein 9/10
 NmB1768: hemagglutinin/hemolysin-related protein 67/27
 NmB1771: hypothetical protein 29/41
 NmB1772: hypothetical protein 16/25
 NmB1829: TonB-dependent receptor 4/32, 47/2
 NmB1830: putative phosphoglycolate phosphatase 4/10
 NmB1854: hypothetical protein 43/48
 NmB1926: *lgtE*, lacto-N-neotetraose biosynthesis glycosyl transferase 79/25
 NmB2132: transferrin-binding protein-related protein 93/5

NmB497 or NmB1779: hemagglutinin/hemolysin-related protein 14/26, 17/21

Figure 2A
(cntd)

Nm2156: *pilD*, prepilin leader peptidase 4/16
 Nm2158: conserved hypothetical protein 1/10
 Nm2159: *pilF*, type IV pilus assembly protein 73/27
 Nm2167: hypothetical protein 1/12
 Nm2168: *emrB*, multidrug resistance translocase 33/39, 57/48
 Nm2171: conserved hypothetical inner membrane protein 4/35, 6/20
 Nm2172: conserved hypothetical protein, possible peptidase 6/38
 Nm2174: conserved hypothetical protein 6/41
 Nm2175: *vapA*, possible virulence associated protein 29/25
 Nm2178: conserved hypothetical protein 2/48
 Nm2180: *aroG*, phospho-2-dehydro-3-deoxyheptonate aldolase 78/10
 Nm2183: *opcB*, outer membrane protein 32/30
 Nm2186: hypothetical protein 19/22
 Nm2189: hypothetical inner membrane protein 2/6', 2/10'
 Nm2193: possible TonB-dependent receptor protein 71/23

 Nm2200: *dinG*, probable ATP-dependent DNA helicase 83/44
 Nm2204: hypothetical protein 1/23, 3/12
 Nm2212: *trpC*, indole-3-glycerol phosphate synthase 83/13
 Nm2216: possible hydrolase 75/11
 Nm2218: possible tRNA/rRNA methyltransferase 1/15
 Nm2223: probable ABC transporter 16/9
 Nm2225: *xseB*, exodeoxyribonuclease small subunit 42/37

 Nm188 or Nm205: *glaA*, glucose-1-phosphate thymidyltransferase 27/38', 35/36', 35/39', 37/2', 58/8
 Nm293 or Nm609: *pilC2* or *pilC1*, pilus-associated protein 5/42
Nm525 or Nm527: *lgtB*, lacto-N-neotetraose biosynthesis glycosyl transferase 3/39
 Nm690 or Nm692: unknown 91/33
 Nm788 or Nm1626: *fpa* or *fpc*, exotoxin 3/17, 4/36', 7/36', 9/1, 13/41, 18/36, 19/7, 21/17'', 24/17'', 27/28, 65/27, 67/22
 Nm1167 or Nm1999: possible phage protein 12/37, 18/37
 Nm1169 or Nm2001: unknown 78/44
 Nm1196 or Nm1310: unknown 8/44
 Nm1186 or Nm1301: unknown 49/23, 56/37
 Nm1313 or Nm1852: unknown 20/16
 Nm1780 or Nm1781: doubtful ORFs 94/44

NmB65: hypothetical protein 61/44, 77/4
 NmB69: *siaB*, polysialic acid capsule biosynthesis protein 28/22
 NmB70: *synX*, polysialic acid capsule biosynthesis protein 77/19
 NmB91: hypothetical protein 1/4
 NmB98: ABC transporter, ATP-binding protein 7/23, 65/6, 69/1
 NmB223: hypothetical protein 30/6
 NmB372: hypothetical protein 84/20
 NmB493: hemagglutinin/hemolysin-related protein 11/1, 12/1
 NmB648: hypothetical protein 5/40
 NmB653: MafB-related protein 12/21
 NmB896: integrase 16/22, 43/15, 94/14
 NmB1502: hypothetical protein 4/3, 76/31
 NmB1603: tellurite resistance protein 28/10
 NmB1759: conserved hypothetical protein 9/10
 NmB1768: hemagglutinin/hemolysin-related protein 67/27
NmB1771: hypothetical protein 29/41
 NmB1772: hypothetical protein 16/25
 NmB1829: TonB-dependent receptor 4/32, 47/2
 NmB1830: putative phosphoglycolate phosphatase 4/10
 NmB1854: hypothetical protein 43/48
NmB1926: *lgtE*, lacto-N-neotetraose biosynthesis glycosyl transferase 79/25
 NmB2132: transferrin-binding protein-related protein 93/5
 NmB497 or NmB1779: hemagglutinin/hemolysin-related protein 14/26, 17/21

Figure 2B

	703,864 Nm715	= 1,221,368	Nm891	1,415,494	repeats		1,568,211
2,126,264	2,105,217 Nm2158	2,088,655 Nm2140	2,112,160 Nm2167	1,767,971 Nm1820	658,297 Nm670	2,172,491 Nm2218	2,074,248
2,084,953		2,054,730 Nm2101		236,709 Nm251	2,123,512	2,153,822	948,069
1,460,109		repeats	886,418 Nm909		repeats	1,460,937 Nm1558	Nm982
				857,399 Nm884	272,128 Nm287	878,672 Nm905	1,238,879 Nm1334
				?	1,951,943 Nm2016	1,521,873	687,649 Nm696
	1,698,665 Nm1756	666,979 Nm679	64,843 Nm70			Nm1617	927,411 Nm962

Pool 1

Figure 2B

	703,864 Nm715	# 1,221,368	NmB91	1,415,494	repeats		1,568,211
2,126,264	2,105,217 Nm2158	2,088,655 Nm2140	2,112,160 Nm2167	1,767,971 Nm1820	658,297 Nm670	2,172,491 Nm2218	2,074,248
2,084,953		2,054,730 Nm2101		236,709 Nm251	2,123,512	2,153,822 Nm2204	948,069 Nm982
1,460,109		repeats	886,418 Nm909		repeats	1,460,937 Nm1558	1,238,879 Nm1334
				857,399 Nm884	272,128 Nm287	878,672 Nm905	687,649 Nm696
	1,698,665 Nm1756	666,979 Nm679	64,843 Nm70	?	1,951,943 Nm2016	1,521,873 Nm1617	927,411 Nm962

POOL 1

Figure 2B (cntd)

685,934	1,698,113 Nm1755	2,045,802 Nm2092	?	2,136,820 Nm2189	2,068,820 Nm2113	1,176,767 Nm1249
1,829,713 Nm1901	2,136,820 Nm2189	1,895,085 Nm1960	# 577,460 Nm602	703,371 Nm714	1,756,638 Nm1812	385,514 Nm414
2,127,931	374,049 Nm2155	2,103,202 Nm2155	?		repeats	1,207,685
	279,824 Nm293	1,818,091 Nm1892	repeats	1,869,663 Nm1937	2,027,616 Nm2078	
	?	?	?	1,810,265	1,020,046 Nm1062	1,910,464 Nm1973
repeats		# 343,864	910,624 Nm941	965,796 Nm1001		2,125,540 Nm2178

Pool 2

Figure 2B (cntd)

685,934	1,698,113 Nm1755		2,045,802 Nm2092	?	2,136,820 Nm2189	2,068,820 Nm2113	1,176,767 Nm1249
1,829,713 Nm1901	2,136,820 Nm2189	1,895,085 Nm1960	1,368,594	# 577,460 Nm602	703,371 Nm714	1,756,638 Nm1812	385,514 Nm414
2,127,931	374,049	2,103,202 Nm2155	1,768,357	?		repeats	1,207,685
	279,824 Nm293	1,818,091 Nm1892	1,147,952	repeats	1,869,663 Nm1937	2,027,616 Nm2078	
	?	?	1,469,783 Nm1565	?	1,810,265	1,020,046 Nm1062	1,910,464 Nm1973
repeats			# 343,864	910,624 Nm941	965,796 Nm1001		2,125,540 Nm2178

POOL 2

Figure 2B (cntd)

568,686	806,502	49,167	2,018,920	1,437,482	2,005,571	503,304
Correia			Nm2069	Nm1541		Nm524
?	1,942,983	1,083,831	2,133,985	1,276,911	# 1,893,655	?
	Nm2009	Nm1136	Nm2204		Nm1958	
?	?	685,663	1,336,951		repeats	674,196
FAP-A, FinC		Nm693			Nm2120	Nm688
754,958	62,408	1,568,177	1,641,852		401,037	repeats
Correia			Nm1709		Nm428	
	repeats		1,343,347	890,346	?	repeats
			Nm1448	Nm915	LgtB1/LgtB2	
repeats		1,237,170	77,675	?	1,653,607	1,584,660
		Nm1331			Nm1722	Nm1665

Figure 2B (cntd)

Pool 3

Figure 2B (cntd)

568,686	806,502	49,167	2,018,920	1,437,482	2,005,571	503,304
Correia			Nm2069	Nm1541		Nm524
?	1,942,983	1,083,831	2,153,985	1,276,911	# 1,893,655	?
	Nm2009	Nm1136	Nm2204		Nm1958	
?	?	685,663	1,336,951		repeats	674,196
FspA/FspC		Nm693			Nm2120	Nm688
754,958	62,408	1,568,177	1,641,852		401,037	repeats
Correia			Nm1709		Nm428	
	repeats		1,343,347	890,346	?	repeats
			Nm1448	Nm915	LgtB1/LgtB2	
repeats		1,237,170	77,675	?	1,653,607	1,584,660
		Nm1331			Nm1722	Nm1665

POOL 3

Figure 2B (cntd)

	349,670	NmB1502	695,383	343,862	1,887,296	684,371	?
1,350,469					Nm1951	Nm692	
Nm1456	NmB1850		1,065,606	2,088,549	1,561,892	1,936,090	2,104,164
419,047				Nm2140	Nm1647		Nm2156
Nm445	?	709,626	931,104		?	1,865,887	379,058
1,362,852		Nm720				Nm1934	Nm409
Nm1467			905,094	1,035,280	1,810,015	?	NmB1829
			Nm935	Nm1087	Nm1886		
338,703	2,107,269	2,115,910	?	55,614	1,261,610	1,094,698	635,555
Nm365		Nm2171	FrpA/FrpC	Nm60	Nm1363	Nm1145	
1,756,874	2,067,856		1,602,529	1,343,457	15,654		
Nm1812	Nm2113		Nm1679	Nm1448	Correia,		

Figure 2B (cntd)

Pool 4

Figure 2B (cntd)

	349,670	NmB1502	695,383	343,862	1,887,296	684,371	?
1,350,469 Nm1456	NmB1830		1,065,606	2,088,549 Nm2140	Nm1951 1,561,892 Nm1647	Nm692 1,936,090	2,104,164 Nm2156
419,047 Nm445	?	709,626 Nm720	931,104		?	1,865,887 Nm1934	379,058 Nm409
1,362,832 Nm1467		?	905,094 Nm935	1,035,280 Nm1087	1,810,015 Nm1886	?	NmB1829
338,703 Nm365	2,107,269	2,115,910 Nm2171	?	55,614 Nm60	1,261,610 Nm1363	1,094,698 Nm1145	635,555
1,756,874 Nm1812	2,067,856 Nm2113		1,602,529 Nm1679	1,343,457 Nm1448	15,654 Correia		

POOL 4


50/142

Figure 2B (cntd)

1,016,505 Nm1056	2,039,081		472,245 Nm485			923,380 Nm955	948,460
?	1,943,994 Nm2010	1,612,586	repeats		595,277 Nm618	932,245 Nm968	?
859,895 Correia	2,054,730 Nm2101	1,820,075			# 1,089,503	1,926,443	
306,288 Nm325	?	?	1,405,189 Nm1507	1,089,647	801,597 Nm820	33,202 Nm39	# 1,465,366
2,051,763 Nm2098	?	1,354,690 Nm1461	214,973 Nm225	1,174,994 Nm1248	83,201 Nm84	1,377,702 Nm1482	NmB648
873,622 Nm904	?	1,204,530 Nm1276	?	?	384,917 Nm414	702,612 Nm714	

Pool 5

Figure 2B (cnfd)

1,016,505 Nm1056	2,039,081		472,245 Nm485			923,380 Nm955	948,460
?	1,943,994 Nm2010	1,612,586	repeats		595,277 Nm618	932,245 Nm968	?
839,895 Correia	2,054,730 Nm2101	1,820,075			# 1,089,503	1,926,443	
306,288 Nm525	?	?	1,405,189 Nm1507	1,089,647	801,597 Nm820	33,202 Nm39	# 1,465,366
	2,051,725 Nm2098	1,354,690 Nm1461	214,973 Nm225	1,174,994 Nm1248	83,201 Nm84	1,377,702 Nm1482	NmB648
873,622 Nm904	?	1,204,530 Nm1276	?	?	384,917 Nm414	702,612 Nm714	

POOL 5

51/142

Figure 2B (cntd)

	1,015,304 Nm1054		1,552,951 Nm1642	786,706 Nm801	911,076 Nm942	repeats	826,894 Nm845
390,345 Nm422	734,004 Nm740	?	487,348 Nm506	repeats	repeats	590,156	812,450
	1,015,309	483,345 Nm503	2,115,983 Nm2171		1,324,691	# 1,481,782 Nm1575	repeats
489,641	1,556,678		976,660 Nm1012	265,362 Nm279	1,187,524	repeats	# 1,465,368
1,156,459 Nm1195	1,635,105 Nm1702	965,302 Nm1001	1,277,441		2,228,347 Nm2172	2,054,513	333,694
2,120,475 Nm2174	1,934,871 Nm1995	463,974 Nm478		704,647 Nm715	614,119 Nm631	860,806 Nm888	1,149,676 Nm1206

Figure 2B (cntd)

Pool 6

Figure 2B (cntd)

?	1,015,304		1,552,951	786,706	911,076	repeats	\$26,894
	Nm1054		Nm1642	Nm801	Nm942		Nm845
390,345	734,004	?	487,348	repeats	repeats	590,156	812,450
Nm422	Nm740		Nm506				
	# 1,013,309	483,345	2,115,983		1,324,691	# 1,481,782	repeats
		Nm503	Nm2171			Nm1575	
489,641	1,536,678		976,660	265,362	1,187,524	repeats	# 1,465,268
			Nm1012	Nm279			
1,136,459	1,633,105	965,302	1,277,441		2,228,347	2,054,513	333,694
Nm1195	Nm1702	Nm1001			Nm2172		
2,120,475	1,934,871	463,974		704,647	614,119	860,806	1,149,676
Nm2174	Nm1996	Nm478		Nm715	Nm631	Nm888	Nm1206

51/142

POOL 6

Figure 2B (cntd)

?	1,015,304 Nm1054		1,552,951 Nm1642	786,706 Nm801	911,076 Nm942	repeats	826,894 Nm845
390,345 Nm422	734,004 Nm740	?	487,348 Nm506	repeats	repeats	590,156	812,450
	# 1,013,309	483,345 Nm503	2,115,983 Nm2171		1,324,691	# 1,481,782 Nm1575	repeats
489,641	1,536,678		976,660 Nm1012	265,362 Nm279	1,187,524	repeats	# 1,465,368
1,136,459 Nm1195	1,633,105 Nm1702	965,302 Nm1001	1,277,441		2,228,347 Nm2172	2,054,513	333,694
2,120,475 Nm2174	1,934,871 Nm1996	463,974 Nm478		704,647 Nm715	614,119 Nm631	860,806 Nm888	1,149,676 Nm1206

POOL 6

52/142

Figure 2B (cntd)

876,733				1,319,200	618,039		1,205,001
Nm905				Nm1421			
722,895	# 785,373	810,111		913,047	1,428,643	1,158,431	631,905
Nm730	Nm800	Nm827		Nm944	Nm1533		Nm646
686,146	343,971	1,820,075	717,665	# 1,973,097	620,285	Nm1898	repeats
Nm694	Nm372		Nm725	Nm2029	Nm636		
554,460	1,170,289	1,338,614	repeats	718,183	997,777	1,370,110	# 1,465,368
Nm580	Nm1243	Fig 5B (suite)			Nm1037	Nm1475	
947,591		1,254,406	?	138,690	1,190,428	14,916	937,945
Nm982		Fig 5B (suite)	Fm A/Fm C	Nm155		Nm18	Nm973
	687,915		481,434	2,075,630	745,727	1,314,152	
	Nm696		Nm499		Nm753	Nm1415	

Pool 7

Figure 2B (cntd)

876,733 Nm905	?		1,319,200 Nm1421	618,039		1,205,001
722,895 Nm730	810,111 Nm827		913,047 Nm944	1,428,643 Nm1533	1,158,431	631,905 Nm646
686,146 Nm694	1,820,075	717,665 Nm725	# 1,973,097 Nm2029	620,285 Nm636	NmB98	repeats
554,460 Nm580	1,038,614 Nm1090	repeats	718,183	997,777 Nm1037	1,370,110 Nm1475	# 1,465,368
947,591 Nm982	1,034,406 Nm1086	?	138,690 Nm155	1,190,428	14,916 Nm18	937,945 Nm973
	687,915 Nm696	481,434 Nm499	2,075,630	745,727 Nm753	1,314,152 Nm1415	

POOL 7

53/142

Figure 2B (cntd)

644	1,352,235	1,445,893	1,499,525	343,862	2,115,836	150,856	1,369,492
Nm12		Nm1547	Nm1592			Nm165	Nm1475
1,642,041		2,044,450	1,828,682	2,115,219	?	150,856	
Nm1709			Nm1900			Nm165	
	1,369,492	1,820,075	1,245,859	507,967	983,878	491,581	1,407,434
	Nm1475			Correia	Nm1022	Nm512	
	1,652,248	2,413,971	2,000,303	666,354	303,392	933,246	1,265,402
	Nm1720	Nm372	Nm2054		Nm319		Nm1366
?	1,269,148	?	1,560,853	1,983,878	1,809,404	1,633,105	873,344
	Nm1369		Nm1646	repeats	Nm1886	Nm1702	Nm904
12,174	958,750	359,833	?	707,683	repeats	807,717	
Nm15	Nm995	Nm1466	Nm1196 or 1310			Nm826	

Pool 8

Figure 2B (cntd)

644	1,352,235	1,445,893	1,499,525	343,862	2,115,836	150,856	1,369,492
Nm2		Nm1547	Nm1592			Nm165	Nm1475
1,642,041		2,044,450	1,828,682	2,115,219	?	150,856	
Nm1709			Nm1900			Nm165	
	1,369,492	1,820,075	1,245,859	507,967	983,878	491,581	1,407,434
	Nm1475			Correia	Nm1022	Nm512	
	1,652,248	343,971	2,000,303	666,354	303,392	933,246	1,265,402
	Nm1720	Nm372	Nm2054		Nm319		Nm1366
?	1,269,148	?	1,560,853	1,983,878	1,809,404	1,633,105	873,344
	Nm1369		Nm1646	repeats	Nm1886	Nm1702	Nm904
12,174	958,750	1,359,833	?	707,683	repeats	807,717	
Nm15	Nm995	Nm1466	Nm1196 or 1310			Nm826	

POOL 8

Figure 2B (cntd)

?				955,198	609,648		441,981
FigA FigC					Nm629		
2,093,221	NmB1759	repeats	# 841,843	1,276,911	644,221	1,339,758	1,878,696
Nm2146		1,755,247	Nm865			Nm1445	
18,431		1,117,688	2,084,938	435,022	886,670	611,115	?
Nm22		Nm1164		Nm457	Nm909	Nm631	
874,549		1,585,203	959,423	repeats	2,054,565		
Nm905		Nm1665	Nm995				
	838,871	1,852,051	798,220	55,167	2,054,319		1,861,837
		Nm1920	Nm817	Nm60	Nm2100		Nm1929
	163,763	892,261	2,042,752	# 1,901,617	1,069,137	1,566,007	1,489,574
	Nm182			Nm1966	Nm1118		Nm1584

Figure 2B (cntd)

Pool 9

Figure 2B (cntd)

?					955,198	609,648		441,981
Fip-V/FipC						Nm629		
2,093,221	NmB1759	repeats	repeats	# 841,843	1,276,911	644,221	1,339,758	1,878,696
Nm2146				Nm865			Nm1445	
18,431				2,084,938	435,022	886,670	611,115	?
Nm22					Nm457	Nm909	Nm631	
874,549				959,423	repeats	2,054,565		
Nm905				Nm995				
	838,871			798,220	55,167	2,054,319		1,861,837
				Nm817	Nm60	Nm2100		Nm1929
	163,763			2,042,752	# 1,901,617	1,069,137	1,566,007	1,489,574
	Nm182				Nm1966	Nm1118		Nm1584

POOL 9

55/142

Figure 2B (cntd)

	503,134 Nm524	1,562,753 Nm1647	610,203 Nm630			1,808,086 Nm1886	?
552,213 Nm382	775,797	?	1,896,645 Nm1961	654,467	420,833 Nm445	1,415,342	1,028,000 Nm1074
1,036,914	722,796 Nm730		1,315,653 Nm1417	682,133 Nm690	1,425,908 Nm1528	2,001,393	747,045
repeats	?	2,100,166	repeats		2,054,565		2,068,748 Nm2113
637,874 Nm650	1,399,195 Nm1483			1,719,627			822,846
	1,307,638 Nm1409	278,168 Nm292	745,346			383,780 Nm413	

Pool10

Figure 2B (cntd)

	503,134 Nm524	1,562,753 Nm1647	610,203 Nm630			1,808,086 Nm1886	?
352,213 Nm382	775,797	?	1,896,645 Nm1961	654,467	420,833 Nm445	1,415,342	1,028,000 Nm1074
1,036,914	722,796 Nm730		1,315,653 Nm1417	682,133 Nm690	1,425,908 Nm1528	2,001,393	747,045
repeats	?	2,100,166	repeats		2,054,565		2,068,748 Nm2113
637,874 Nm650	1,379,195 Nm1483			1,719,627			822,846
	1,307,638 Nm1409	278,168 Nm292	745,346			383,780 Nm413	

POOL 10

Figure 2B (cntd)

Nm13493	349,670		1,614,134 Nm1690	851,590 Nm873		232,002 Nm247	420,833 Nm445
Nm518	2,052,437 Nm2099	1,459,278 Nm1557	1,262,685 Nm1363	1,027,428 Nm1073	2,086,269 Nm2137	1,696,334	232,000 Nm247
# 483,902	1,990,827	1,857,005	1,646,465	?	947,390	1,605,658	718,555
Nm503	Nm2046	Nm1925	Nm1715		Nm981		Nm726
1,082,663	747,103	1,354,680	572,705	?	1,395,005	1,292,265	1,277,299
Nm1134		Nm1460	Nm600			Nm1393	Nm1373
639,823		1,478,537		?	1,253,541	?	
Nm654		Nm1574			Nm1356		
1,107,042	2,086,269 Nm2137	repeats	1,892,121 Nm1957	1,123,351 Nm1174			

Pool 11

Figure 2B (cntd)

Nm1493	349,670		1,614,134 Nm1690	851,590 Nm873		232,002 Nm247	420,833 Nm445
# 799,823 Nm818	2,052,437 Nm2099	1,459,278 Nm1557	1,262,685 Nm1363	1,027,428 Nm1073	2,086,269 Nm2137	1,696,334	232,000 Nm247
# 483,902 Nm503	1,990,827 Nm2046	1,857,005 Nm1925	1,646,465 Nm1715	?	947,390 Nm981	1,605,658	718,555 Nm726
1,082,665 Nm1134	747,103	1,354,680 Nm1460	572,705 Nm600	?	1,395,005	1,292,265 Nm1393	1,277,299 Nm1373
659,823 Nm654		1,478,537 Nm1574		?	1,253,541 Nm1356	?	
1,107,042	2,086,269 Nm2137	repeats	1,892,121 Nm1957	1,123,351 Nm1174			

POOL 11

Figure 2B (cnld)

NmB493	1,911,190	repeats	209,739	1,483,767	236,618	786,706
	Nm1973		Nm221	Nm1577	Nm251	Nm801
repeats	1,165,235		298,612		1,253,625	
	Nm1234				Nm1356	
236,490	1,132,888	236,618	NmB653		?	1,941,704
Nm251	Nm1186	Nm251				Nm2007
415,186		?		2,051,828	1,306,890	2071193
Nm441				Correia	Nm1408	Nm2118
				repeats	1,057,731	
	878,949	1,767,075	?		Nm1110	
	Nm905	Nm1819	Nm1167Nm1999			
		1,808,168	741,849	1,245,699	2,060,827	
		Nm1886	Nm750	Nm1341		

Pool 12

Figure 2B (cntd)

NimB493	1,911,190 Nm1973	repeats		209,739 Nm221	1,483,767 Nm1577	236,618 Nm251	786,706 Nm801
repeats	# 1,165,235 Nm1234			298,612		1,253,625 Nm1356	
236,490 Nm251	1,132,888 Nm1186	236,618 Nm251		NmB653		?	1,941,704 Nm2007
415,186 Nm441		?	298,306 Nm307		2,051,828 Correia	1,306,890 Nm1408	207,193 Nm2118
	878,949 Nm905	1,767,075 Nm1819	341,230 Nm368	?	repeats	1,057,731 Nm1110	
		1,808,168 Nm1886		741,849 Nm750	1,245,699 Nm1341	2,060,827	

POOL 12

Figure 2B (cntd)

	2,025,485 Nm2076			1,301,518 Nm1401	994,646 Nm1034	1,103,757 Nm1152	
	2,082,006 Nm2131		1,097,438	repeats	repeats		180,821 Nm198
		390,462 Nm422	1,809,978 Nm1886				
745,160				# 2,071,060 Nm2117	# 1,679,952 Nm1740	139,199 Nm155	# 1,465,368
366,813 Nm397		1,852,051 Nm1920	repeats	92,107		1,380,378 Nm1485	
	2,032,849 Nm2084	303,532 Nm320	1,414,499 Nm1519			62,001	
FrpA C							

Pool 13

Figure 2B (cntd)

	2,025,485			1,301,518	994,646	1,103,757	
	Nm2076			Nm1401	Nm1034	Nm1152	
	2,082,006		1,097,438	repeats	repeats		180,821
	Nm2131						Nm198
			390,462				
			Nm422				
			1,809,978				
			Nm1886				
745,160	?			# 2,071,060	# 1,679,952	139,199	# 1,465,368
				Nm2117	Nm1740	Nm155	
366,813		1,852,051	repeats	92,107		1,380,378	
Nm397		Nm1920				Nm1485	
?	2,032,849	303,532	1,414,499			62,001	
Firpa/C	Nm2084	Nm320	Nm1519				

POOL 13

Figure 2B (cntd)

		1,390,528 Nm1491	1,560,805 Nm1646			709,875 Nm720	1,184,706 Nm1255
1,417,135		1,378,089 Nm1483			2,054,792 Nm2101		
						1,696,173 Correia	1,152,464 Nm1207
567,352 Nm594	NmB497α 1779			815,550 Nm832		675,200 Nm688	297,511
745,160		1,697,450 Nm1754	948,460	1,520,153		1,301,518 Nm1401	1,401,731
	1,083,772 Nm1136		1,290,607	2,102,277 Nm2155	70,533 Nm73	?	417,289

Pool 14

Figure 2B (cntd).

		1,390,528 Nm1491	1,560,805 Nm1646			709,875 Nm720	1,184,706 Nm1255
1,417,135		1,378,089 Nm1483			2,054,792 Nm2101		
						1,696,173 Correia	1,152,464 Nm1207
567,352 Nm594				815,550 Nm832		675,200 Nm688	297,511
745,160		1,697,450 Nm1754	948,460	1,520,153		1,301,518 Nm1401	1,401,731
			1,290,607	2,102,277 Nm2155	70,533 Nm73	?	417,289
		1,083,772 Nm1136					

POOL 14

Figure 2B (cntd)

973,938 Nm1008	2,073,448			1,495,207 Nm1590	1,332,096 Nm1438		1,972,429
214,969 Nm225	1,698,716 Nm1756	1,084,893	1,858,309	# 541,225 Nm567	62,406	2,075,433	782,166
666,947 Nm679		1,232,670 Nm1325	175,446 Nm193	223,973	611,239 Nm631	77,675	1,099,411 Nm1149
	1,032,157 Nm1084						472,929 Nm486
	?	1,366,559 Nm1473	1,611,297 Nm1687				704,647 Nm715
			?			31,414	1,381,289 Nm1485

Pool 15

Figure 2B (cntd)

973,938 Nm1008	2,075,448			1,495,207 Nm1590	1,332,096 Nm1438		1,972,429
214,969 Nm225	1,698,716 Nm1756	1,084,893	1,858,309	# 541,225 Nm567	62,406	2,075,433	782,166
666,947 Nm679		1,232,670 Nm1325	175,446 Nm193	223,973	611,239 Nm631	77,675	1,099,411 Nm1149
	1,032,157 Nm1084						472,929 Nm486
	?	1,366,559 Nm1473	1,611,297 Nm1687				704,647 Nm715
			?			31,414	1,381,289 Nm1485

POOL 15

Figure 2B (cntd)

274,161	674,198		239,262	1,095,984	
Nm289	Nm688		Nm255	Nm1148	
2,176,234	2,033,365	repeats	1,204,534	# 625,143	?
Nm223	Nm2084		Nm1276	Nm639	
# 483,902		219,573	1,870,725	NmB896	
Nm503		Nm233	Nm1938		
NmB1772	?			# 2,074,494	repeats
				Nm2123	
7,561	1,068,213	FrpA/C	1,295,073	957,570	
Nm10			Nm1395	Nm994	
	1,106,063		472,082		
		1,979,533	Nm485		
		Nm2038			

Pool 16

Figure 2B (cntd)

274,161 Nm289	674,198 Nm688			239,262 Nm255	1,095,984 Nm1148		
2,176,234 Nm223	2,033,365 Nm2084		repeats	1,204,534 Nm1276		# 625,143 Nm639	?
# 483,902 Nm503			219,573 Nm233	1,870,725 Nm1938	NmB896		
NmB1772					# 2,074,494 Nm2123	# 928,376	repeats
7,561 Nm10	1,068,213	FipA/C		1,295,073 Nm1395		957,570 Nm994	
		1,106,063	1,979,533 Nm2038	472,082 Nm485			

POOL 16

Figure 2B (cntd)

			178,647 Nm195	1,810,615 Nm1887		1,892,522 Nm1957
		70,176 Nm73				2,038,918
			?			
			Nm13497 or 1779			
			948,920	?	1,833,197	2,157,77
335,167						

Pool 17

Figure 2B (cntd)

			178,647 Nm195	1,810,615 Nm1887		1,892,522 Nm1957
		70,176 Nm73				2,038,918
			?			
			NmB497 α 1779			
			948,920	?	1,833,197	2,157,77
335,167						

POOL 17

Figure 2B (cntd)

		1,009,610 Nm1048				?
792,595			363,135	1,222,899 Nm1313	178,647 Nm195	753,229 Nm762
		1,059,662 Nm1111	618,007	1,307,751 Nm1409	298,638	
1,413,590 Nm1518	?		1,880,098 Nm1946		1,225,309 Nm1315	1,810,158
346,481 Nm374	2,002,551		FipA/FipC	? Nm167Nm1999	1,867,553 Nm1934	
Repeats			1,095,057 Nm1146		153,926 # 1,859,121	40,553 Nm48

Pool 18

Figure 2B (cntd)

		1,009,610 Nm1048					?
792,595			363,135	1,222,899 Nm1313		178,647 Nm195	753,229 Nm762
		1,059,662 Nm1111	618,007	1,307,751 Nm1409		298,638	
1,413,590 Nm1518	?		1,880,098 Nm1946			1,225,309 Nm1315	1,810,158
346,481 Nm374	2,002,551		FtpA/FtpC	?	346,481 Nm374	1,867,553 Nm1934	
repeats			1,095,057 Nm1146		153,936	# 1,859,121	40,553 Nm48

POOL 18

Figure 2B (cntd)

166,036	repeats		1,418,510	1,177,109	1,328,654	FipA/C	796,864
Nm184			Nm1523	Nm1250	Nm1435		Nm816
	1,476,286		1,039,018	236,490	168,270		311,848
			Nm1090	Nm251	Nm185		
1,429,574		746,538	333,579	# 1,406,958	2,129,971		854,264
		Nm753		Nm1508	Nm2186		Nm879
1,605,658		745,076		1,264,321			
		Nm752		Nm1365			
639,823	1,353,165		555,530	1,397,846		1,717,473	
Nm654	Nm1459		Nm582	Nm1500		Nm1771	
		147,988	60,962	2,091,395	repeats		1,484,721
		Nm162	Nm65	Nm2145			Nm1579

Pool 19

Figure 2B (cntd)

166,036 Nm184	repeats		1,418,510 Nm1523	1,177,109 Nm1250	1,328,654 Nm1435	FipA/C	796,864 Nm816
	1,476,286		1,039,018 Nm1090	236,490 Nm251	168,270 Nm185		311,848
1,429,874		746,538 Nm753	333,579	# 1,406,938 Nm1508	2,129,971 Nm2186		854,264 Nm879
1,605,658		745,076 Nm752		1,264,321 Nm1365			
639,823 Nm654	1,353,165 Nm1459		555,530 Nm582	1,397,846 Nm1500		1,717,473 Nm1771	
		147,988 Nm162	60,962 Nm65	2,091,395 Nm2145	repeats		1,484,721 Nm1579

POOL 19

Figure 2B (cntd)

1,490,525 Nm1592		repeats	325,573 Nm348			18,989 Nm24	1,633,760
523,612 Nm546				2,073,687 Nm2122	1,654,150	390,345 Nm422	?
	931,104	1,870,638 Nm1937					76,633 Nm77
		683,971 Nm692		repeats			
	1,095,984 Nm1148	1,417,135					1,204,632 Nm1276
			16,188 Nm20				

Pool 20

Figure 2B (cntd)

1,499,525 Nm1592		repeats	325,573 Nm348		18,989 Nm24	1,633,760
523,612 Nm546				2,073,687 Nm2122	390,345 Nm422	?
	931,104	1,870,638 Nm1937				76,633 Nm77
		683,971 Nm692		repeats		
	1,095,984 Nm1148	1,417,135				1,204,632 Nm1276
			16,188 Nm20			

POOL 20

Figure 2B (cntd)

[illegible]

200712

Figure 2B (cntd)

POOL 21

Figure 2B (cntd)

	1,577,038 Nm1660			1,830,389 Nm1901			
		681,430 Nm690			168,270 Nm185		
	1,221,839 Nm1313	repeats					
1,236,888 Nm1531							
			543,611	repeats			
				328,357 Nm353			?

Pool 22

Figure 2B (cntd)

	1,577,038 Nm1660		1,830,389 Nm1901			
		681,430 Nm690		168,270 Nm185		
	1,221,839 Nm1313	repeats				
1,236,888 Nm1331						
			repeats			
		543,611				
			328,357 Nm353			?

POOL 22

Figure 2B (cntd)

Figure 2B (cntd)

[illegible]

POOL 23

Figure 2B (cntd)

				repeats			
				2,027,698			33,147
				Nm2078			Nm39
FtpA CtpC							1,204,377

Pool 24

70 1142

Figure 2B (cntd)

				965,907 Nm1001	175,369 Nm193		
168,597 Nm185				repeats	978,564 Nm1015		1,520,153
			2,102,998 Nm2155			1,260,973 Nm1362	
1,408,644 Nm1509							
							# 1,857,813 Nm1925
				139,199 Nm155			

Pool 25

Figure 2B (cntd)

163,597				965,907 Nm1001	175,369 Nm193		
Nm185				repeats	978,564 Nm1015		1,520,153
			2,102,998 Nm2155			1,260,973 Nm1362	
1,408,644 Nm1509							
							# 1,857,813 Nm1925
				139,199 Nm155			

POOL 25

Figure 2B (cntd)

		1,117,429 Nm1163					
					7,797 Nm10	969,041	

Pool 26

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1st filing

Figure 2B (cntd)

		1,117,429 Nm1163					
						7,797 Nm10	969,041

POOL 26

27

[illegible]

[illegible]

POOL 27

28

[illegible]

Figure 2B (cntd)

Figure 2B (cntd)

		2,073,103 Nm2122			1,729,621 Nm1786		?
2,122,885 Nm2173			785,375 Nm800			977,978 Nm1015	
NmB1771	968,313 Nm1003	1,044,730	# 14,356 Nm17				

Pool 29

Figure 2B (cntd)

		2,073,103 Nm2122			1,729,621 Nm1786	?
2,122,865 Nm2175			785,375 Nm800			977,978 Nm1015
NmB1771	968,513 Nm1003	1,044,730	# 14,356 Nm17			

POOL 29

				NimB223			
= 1,190,683				repeats			
786,864							
Nim802							
2,031,496							
Nim2083							

Pool 30

					NmB223			
# 1,190,685					repeats			
786,864								
Nm802								
2,031,496								
Nm2083								

POOL 30

Figure 2B (cntd)

Figure 2B (cntd)

[illegible]

POOL 31

[illegible]

2007 32

[illegible]

POOL 32

Figure 2B (cntd)

911,904						2,084,904	
Nm942							
						2,113,660	
						Nm2168	
						349,670	
							1,515,641

Tool 33

Figure 2B (cntd)

	911,904 Nm942					2,084,904	
						2,113,660 Nm2168	
					349,670		1,515,641

POOL 33

Figure 2B (cntd)

1,851,986 Nm1920		1,204,052			1,056,116 Nm1108	1,151,839 Nm1206
611,024 Nm631	# 319,551			1,612,668		
	1,413,502 Nm1518	1,315,330 Nm1417				

Pool 34

Figure 2B (cntd)

1,851,986 Nm1920		1,204,052			1,056,116 Nm1108	1,151,839 Nm1206
611,024 Nm631	# 319,551			1,612,668		
	1,413,502 Nm1518	1,315,330 Nm1417				

POOL 34

[illegible]


Pool 35

Figure 2B (cntd)

1,723,027 Nm1778							
	1,754,153 Correia						
2,711 Nm3						735,966 Correia	
					1,008,897 Nm1048	?	
					Nm188 or 205		
		410,874					

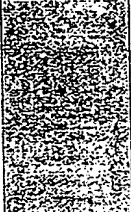
POOL .35

Figure 2B (cntd).

	810,726 Nm828	1,819,643 Nm1894	812,142			
		repeats		1,681,423		
		1,906,710 Nm1969	1,397,846 Nm1500			

Pool 36

Figure 2B (cntd)

		810,726 Nm828	1,819,643 Nm1894	812,142			
			repeats		1,681,423		
			1,906,710 Nm1969	1,397,846 Nm1500			

POOL 36

Figure 2B (cntd)

	Nm188 or 205								
1,680,042 Nm1740									
						985,021 Nm1022			
1,924,258 Nm1984								1,887,137 Nm1951	

Pool 37

Figure 2B (cntd)

	?								
	Nm188 or 205								
1,680,042									
Nm1740									
					985,021				
					Nm1022				
1,924,258								1,887,137	
Nm1984								Nm1951	

POOL 37

Figure 2B (cntd)

271,212									
Nm285									
									801,367 Correia
								2,054,741 Nm2101	2,067,769 Nm2113
# 1,996,593							repeats		
Nm2052									

Pool 38

[illegible]

POOL 38

Figure 2B (cntd)

		871,236		258,675			
				Nm274			

Pool 39

[illegible]

POOL 39

Figure 2B (cntd).

					# 1,089,534	1,425,794 Nm1528		
				repeats		1,561,122 Nm1646		
							437,722 Nm457	
1,272,492 Nm1371						1,350,097 Nm1456		
					180,812			

POOL 40

[illegible]

Root 42

1

1

1

Pool 42

[illegible]

Figure 2B (cntd)

[illegible]

POOL 42

Figure 2B (cntd)

			1,442,807 Nm1545	2,075,312 Nm2124		181,807 Nm198
1,013,296 Nm1052			1,946,913 Nm2012	629,259 Nm643	NmB896	
1,238,616 Nm1334	1,426,582					
						NmB1854

Tool 13

Figure 2B (cntd)

				1,442,807 Nm1545	2,075,312 Nm2124		181,807 Nm198
1,013,296 Nm1052				1,946,913 Nm2012	629,259 Nm643	NmB896	
1,238,616 Nm1334		1,426,582					
							NmB1854

POOL 43

Figure 2B (cntd)

[illegible]

POOL 44

Figure 2B (cntd)

					repeats		
	1,494,806 Nm1598				777,623		
	503,208 Nm524						

Pool 45

[illegible]

POOL 45

Figure 2B (cntd)

927,175		1,290,609		325,831 Nm349	
			856,389		
1,478,500 Nm1574	846879 Nm868				
	350,939 Nm380	596,375 Nm619	1,076,184 Nm1126	2,090,752 Nm2142	
	342,700 Nm370		682,470 Nm691		

2006 46

Figure 2B (cntd).

927,175		1,290,609		325,831 Nm349	
			856,389		
1,478,600 Nm1574	846879 Nm868				
	350,939 Nm380	596,375 Nm619	1,076,184 Nm1126	2,090,752 Nm2142	
	342,700 Nm370		682,470 Nm691		

POOL 46

Figure 2B (cntd)

NmB18-9		1,866,786 Nm1934		398,054 Nm425	
565,358 Nm592		258,675 Nm274	597,736 Nm619		
	1,139,697 Nm1200			2,045,558 Nm2092	
	1,028,178 Nm1074				
		1,870,396 Nm1937	573,776 Nm601	997,525 Nm1037	
	2,481			142,042 Nm157	

Pool 47

Figure 2B (cntd)

Figure 2B (cntd)

1,117,429 Nm1163	2,008,688		# 845,850 Nm867	675,145 Nm688	
		repeats			
	815,746 Nm832				

POOL 48

Figure 2B (cntd)

[illegible]

2007

Figure 2B (cntd)

						1,852,520 Nm1920	2,079,897 Nm2129	
						229,743		
1,944,454 Nm2010							?	
						62,096 Nm67		
?						812,107		2,123,497
repeats								

POOL 49

Figure 2B (cntd)

[illegible]

200705

Figure 2B (cntd)

POOL 50

Figure 2B (cntd)

		1,726,253 Nm1783				?		
						746,768 Nm753		
	?					718,075 Nm725		
	repeats							
		156,537 Nm173						?

Pool 51

Figure 2B (cnfd)

		1,726,253 Nm1783				?		
						746,768 Nm753		
	?					718,075 Nm725		
		156,537 Nm173						?
?								

POOL 51

Figure 2B (cntd)

785,007 Nm800	?		2,037,927	# 2,079,961 Nm2130	?	
1,352,657 Nm1459	825,538	1,139,697 Nm1200				
			1,709,975 Nm1765			

Pool 52

Figure 2B (cntd)

785,007 Nm800		?		2,057,927	# 2,079,961 Nm2130	?	
1,352,657 Nm1459	825,538	repeats	1,139,697 Nm1200				
		?		1,709,975 Nm1765			

POOL 52

Figure 2B (cntd)

Figure 2B (cntd)

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Figure 2B (cntd).

[illegible]

Pool 54

Figure 2B (cntd)

?					

POOL 54

Figure 2B (cntd)

[illegible]

POOL 55

Figure 2B (cntd)

	?					
?	?	repeats				
	927,430	Nm962			1,977,980	Nm2036
	825,132	Nm843		?		
				Nm1186/Nm1301		
					1,406,960	Nm1508

Pool 56

Figure 2B (cntd)

	?								
?	?	repeats							
	927,430	Nm962					1,977,980	Nm2036	
	825,132	Nm843				?			
						Nm1186/Nm1301			
						1,406,960			
						Nm1508			

POOL 56

[illegible]

53

Figure 2B (cntd)

						1,870,396 Nm1937			
	165,931 Nm184	1,893,893 Nm1958					538,192 Nm560		
1,520,208									
14,463 Nm17					?	Correia	555,097 Nm582		
								2,113,675 Nm2168	

POOL 57

Figure 2B (cntd)

			1,853,253 Nm1921			?

Pool 58

[illegible]

POOL 58

Figure 2B (cntd)

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Figure 2B (cntd)

				866,234 Nm892					
		1,878,224 Nm1944							
						43,350 Nm50			
994,369 Nm1035						351,042			
								160,326	

Pool 60

Figure 2B (cntd)

			866.234 Nm892				
	1,878.224 Nm1944						
					43,350 Nm50		
994.969 Nm1035					351,042		
						160.326	

POOL 60

Figure 2B (cntd)

		474,594	409,823			
		Nm489	Nm434			
			1,633,760		826,623	
		NmB65			1,547,033	Nm1639

Pool 61

Figure 2B (cntd)

[illegible]

POOL 61

Figure 2B (cntd)

[illegible]

2007-62

[illegible]

POOL 62

Figure 2B (cntd)

				1,268,930 Nm1369				
				1,435,284 Nm1540	?			
						1,870,199 Nm1937		

Pool 63

Figure 2B (cntd)

				1,268,930 Nm1369				
				1,435,284 Nm1540	?			
						1,870,199 Nm1937		

POOL 63

Figure 2B (cntd)

			950,279 Nm987	?			
		?					
		repeats					
			14,916 Nm18				

Pool 64

Figure 2B (cntd)

			950,279 Nm987	?			
		?					
		repeats					
			14,916 Nm18				

POOL 64

[illegible]

2005

Figure 2B (cntd)

						NmB98			
2,144,642 Nm2196				?	repeats				
1,276,053 Nm1372				1,820,075					
				?	FrpA/TipC				
								1,068,603 Nm1118	
								854,264 Nm879	

POOL 65

Figure 2B (cntd)

[illegible]

POOL 66

[illegible]

60

[illegible]

POOL 67

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Figure 2B (cntd)

repeats	1,346,136 Nm1450							
		919,190 Nm952					# 1,074,971	
						534,919 Nm559	2,071,324 Nm2118	
623,563 Nm638								
?								

Pool 68

Figure 2B (cntd)

repeats	1,346,136 Nm1450						
		919,190 Nm952				# 1,074,971	
					534,919 Nm559	2,071,324 Nm2118	
623,563 Nm638							
?							

POOL 68

Figure 2B (cntd)

1451,507					NmB98			
					785,693 Nm800			
						659,299 Nm672		

Pool 69

Figure 2B (cntd)

1,451,507					NmB98			
					785,693 Nm800			
					659,299 Nm672			

POOL 69

[illegible]

2007

Figure 2B (cntd)

Figure 2B (cntd)

	446,234 Nm465				748,149 Nm755	1,089,024 Nm1140	1,893,893 Nm1958
?	1,893,893 Nm1958		1,207,721				1,286,858
	480,137 Nm497	39,237 Nm47				2,142,378 Nm2193	
1,245,859					repeats		
		1,868,210 Nm1936				?	
		?	repeats				

200L 71

Figure 2B (cntd)

	446,234 Nm465			748,149 Nm755	1,089,024 Nm1140	1,893,893 Nm1958
?	1,893,893 Nm1958	1,207,721				1,286,858
	480,137 Nm497	39,257 Nm47			2,142,378 Nm2193	
1,245,859				repeats		
					?	
			repeats			

POOL 71

[illegible]

2007-2

Figure 2B (cntd)

				1,286,858	637,868 Nm650		
						9	
957388 Nm993							164,476 Nm183

POOL 72

[illegible]

2873

Figure 2B (cntd)

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Figure 2B (cntd)

[illegible]

Pool 74

Figure 2B (cntd)

[illegible]

POOL 74

Figure 2B (cntd).

[illegible]

700 SF

Figure 2B (cntd)

[illegible]

700797

Figure 2B (cntd)

							264,485 Nm279		
1,084,893 Nm1136						1,248,598 Nm1348	1,282,003		
							1,858,309		
							1,908,190 Nm1970	NmB1502	
						1,251,524 Nm1351			
						263,064		1,654,334	

POOL 76

			NimB65			
			1,499,525 Nim1592	?		
1,149,317 Nim1206	390,879 Nim422	NimB70				

200

Figure 2B (cntd)

				NmB65			
				1,499,525 Nm1592	?		
1,149,317 Nm1206	390,879 Nm422	NmB70					

POOL 77

[illegible]

2878

Figure 2B (cntd)

Figure 2B (cntd).

[illegible]

57 782

Figure 2B (cntd)

[illegible]

POOL 79

Figure 2B (cntd)

952,888 Nm990		169,996 Nm186	1,704,036 Nm1761			
		1,235,126			1,808,405 Nm1886	
					1,889,562 Nm1953	81,787 Nm83
		# 669,444	55,614 Nm60			

Pool 80

Figure 2B (cnld)

	952,888 Nm990		169,996 Nm186	1,704,036 Nm1761				
			1,235,126				1,808,405 Nm1886	
						1,889,562 Nm1953	81,787 Nm83	
			# 669,444	55,614 Nm60				

POOL 80

Figure 2B (cntd)

[illegible]

200

Figure 2B (cntd)

		?	1,991,435				
		repeats	Nm2048				
						341,653	
						Nm369	
							1,994,152

POOL 81

Pool 82

[illegible]

[illegible]

POOL 82

Figure 2B (cntd)

				1,487,405		1,027,590 Nm1073	
				2,166,913 Nm2212			
				2,148,926 Nm2200			

Pool 83

Figure 2B (cntd)

				1,487,405		1,027,590 Nm1073	
				2,166,913 Nm2212			
					2,148,926 Nm2200		

POOL 83

Figure 2B (cntd)

?	345,511 Nm374					
1,035,282 Nm1087		NmB372				

Pool 84

Figure 2B (cntd)

?	345,511 Nm374						
1,035,282 Nm1087			NmB372				

POOL 84

Figure 2B (cntd)

[illegible]

POOL 85

Figure 2B (cntd)

168,432 Nm185			1,404,807 Nm1507				
					2,039,301 Nm2086		
				1,853,253 Nm1921			

POOL 86

Figure 2B (cntd)

[illegible]

POOL 87

Figure 2B (cntd).

[illegible]

208

[illegible]

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Figure 2B (cntd).

[illegible]

287

Figure 2B (cntd)

[illegible]

POOL 89

[illegible]

90

Figure 2B (cntd)

[illegible]

POOL 90

Figure 2B (cntd) :

	571,814 Nm599	1,321,363 Nm1425				
1,613,820 Nm1689					1,443,339	
				2,000,734 Nm2054		
?						?
Nm690 or 692						
595,277 Nm618		2,109,838			289,906	

Pool 91

Figure 2B (cnld)

	571,814 Nm599	1,321,363 Nm1425				
1,613,820 Nm1689					1,443,339	
				2,000,734 Nm2054		
?						?
Nm690 or 692						
595,277 Nm618		2,109,838			289,906	

POOL 91

237/142

Figure 2B (cntd)

	780,313 Nm796		976,649 Nm1012	1,369,405 Nm1475			
2,085,389 Nm2136	148,703	243,185 Nm259	1,369,405 Nm1475	1,558,864 Nm1645		734,251 Nm741	
	1,956,664 Nm2020			1,767,251 Nm1819	1,269,498 Correia	1,092,318 Nm1143	
# 206,285 Nm220		1,183,770 Nm1255	1,239,706	# 1,086,735 Nm1139		repeats	1,290,609
		142,196	144,763 Nm160				
590,283 Nm613	1,907,294 Nm1970	721,054 Nm729	# 1,369,654 Nm1475	595,277 Nm618			

Pool 92

Figure 2B (cntd)

	780,313 Nm796		976,649 Nm1012	1,369,405 Nm1475			
2,085,389 Nm2136	148,703	243,185 Nm259	1,369,405 Nm1475	1,558,864 Nm1645	734,251 Nm741		
	1,956,664 Nm2020			1,767,251 Nm1819	1,269,498 Correia	1,092,318 Nm1143	
# 200,285 Nm220		1,183,770 Nm1255	1,239,706	# 1,086,735 Nm1139	repeats	1,290,609	
		142,196	144,763 Nm160				
590,283 Nm613	1,907,294 Nm1970	721,054 Nm729	# 1,369,654 Nm1475	595,277 Nm618			

POOL 92

138/142

Figure 2B (cnid)

?	repeats	62,404	?	NmB2132			24,221 Nm29
?	1,225,330 Nm1315	994,900 Nm1035	1,763,435 Nm1816	33,002	1,287,708 Nm1385	1,658,462	repeats
491,378	1,103,537 Nm1152	170,104 Nm186					
788,206 Nm804		?		1,331,057	422,265	866,358	412,800 Nm436
1,860,457 Nm1928	618,039		?	?	217,751 Nm229		849,737
	1,648,062	239,013 Nm255	979,379 Nm1016	625,475 Nm639	1,720,495 Nm1775	178,214 Nm195	?

Pool 93

Figure 2B (cntd)

?	repeats	62,404	?	NmB2132			24,221 Nm29
?	1,225,330 Nm1315	994,900 Nm1035	1,763,435 Nm1816	33,002	1,287,708 Nm1385	1,658,462	repeats
491,378	1,103,537 Nm1152	170,104 Nm186					
788206 Nm804		?		1,331,057	422,265	866,358	412,800 Nm436
1,860,457 Nm1928	618,039		?	?	217,751 Nm229		849,737
	1,648,062	239,013 Nm255	979,379 Nm1016	625,475 Nm639	1,720,495 Nm1775	178,214 Nm195	?

POOL 93

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Figure 2B (cntd)

	966,344 Nm1001						1,068,488 Nm1118
1,915,903 Nm1975					NmB896	1,184,157 Nm1255	
314,780	967,255 Nm1002	1,873,509 Nm1940				265,540	1,257,099
	1,080,375	1,664,669 Nm1731	279,302 Nm293			1,101,935	2,179,156
		1,222,561 Nm1313	1,945,709 Nm2011	# 1,211,124 Nm1285	236,897 Nm251	# 575,138 Nm602	?
?			1,725,097 Nm1780 or 1781		?	1,859,281	1,413,563 Nm1518

Pool 94

Figure 2B (cntd)

	966,344 Nm1001						1,068,488 Nm1118
1,915,903 Nm1975					NmB896	1,184,157 Nm1255	
314,780	967,253 Nm1002	1,873,509 Nm1940				265,540	1,257,099
	1,080,375	1,664,669 Nm1731	279,302 Nm293			1,101,935	2,179,156
		1,222,561 Nm1313	1,945,709 Nm2011	# 1,211,124 Nm1285	236,897 Nm251	# 575,138 Nm602	?
?			1,725,097 Nm1780 or 1781		?	1,859,281	1,413,563 Nm1518

POOL 94

140/142

Figure 2B (cntd)

	1,200,238 Nm1272	2,042,752	827,895 Nm847	1,103,507 Nm1152		1,280,372 Nm1375
898,986 Nm928	1,867,841 Nm1935	?	392,893	291,442 Nm298		#319,551
489,643					151,594 Nm165	
#1,357,825 Nm1465	?					1,219,964 Nm1307
1,981,237 Nm2040		1,945,709 Nm2011	32,210 Nm37		863,804 Nm890	
			745,456 Nm753	?	265,348 Nm279	1,559,590 Nm1646

Pool 95

Figure 2B (cntd)

	1,200,238 Nm1272		2,042,752	827,895 Nm847	1,103,507 Nm1152		1,280,372 Nm1375
898,986 Nm928	1,867,841 Nm1935	?		392,893	291,442 Nm298		#319,551
489,643						151,594 Nm165	
#1,337,825 Nm1465	?						1,219,964 Nm1307
1,981,237 Nm2040			1,945,709 Nm2011	32,210 Nm37		863,804 Nm890	
				745,456 Nm753	?	265,348 Nm279	1,559,590 Nm1646

POOL 95

141 / 142

Figure 2B (cntd)

1,116,609 Nm1162	1,085,727 Nm1138	654,474	1,729,378 Nm1786		?	1,056,050 Nm1107
	1,487,870	596,933 Nm619	1,509,295 Nm1603		1,728,474 Nm1785	927,970 Nm962
	?		2,038,850	475,258 Nm490	572,193 Nm599	1,654,720 Nm1723
1,390,936				2,000,669 Nm2054	800,429 Nm819	618,041
	1,713,480 Nm1767	351,040	?	1,917,966	744,040 Nm752	1,438,987 Nm1542
			repeats	672,238 Nm687	2,086,387 Nm2137	1,559,479

Pool 96

Figure 2B (cntd)

1,116,609 Nm1162	1,085,727 Nm1138	654,474		1,729,378 Nm1786		?	1,056,050 Nm1107
	1,487,870	596,933 Nm619		1,509,295 Nm1603		1,728,474 Nm1785	927,970 Nm962
	?			2,038,850	475,258 Nm490	572,193 Nm599	1,654,720 Nm1723
1,890,936					2,000,669 Nm2054	800,429 Nm819	618,041
	1,713,480 Nm1767	351,040	?	?	1,917,966	744,040 Nm752	1,438,987 Nm1542
			repeats		672,238 Nm687	2,086,387 Nm2137	1,559,479

POOL 96

List of genes important for resistance to the bactericidal action of the complement.

Nm83: dxr, probable 1-deoxy-D-xylulose 5-phosphate reductoisomerase

Nm185: lipB, capsule polysaccharide modification protein

Nm186: lipA, capsule polysaccharide modification protein

Nm195: ctrD, probable capsule polysaccharide export ATP-binding protein

just ahead Nm197: ctrB capsule polysaccharide export inner-membrane protein

Nm198: ctrA, capsule polysaccharide export outer membrane protein

Nm229: unknown

Nm356: possible transferase

Nm524: lgtA, lacto-N-neotetraose biosynthesis glycosyl transferase

Nm525 or Nm527: lgtB or lgtB2, lacto-N-neotetraose biosynthesis glycosyl transferase

Nm848: galU, probable UTP-glucose-1-phosphate uridylyltransferase

Nm1001: pgm, phosphoglucomutase

Nm1034: rfaE, probable ADP-heptose synthetase

Nm1037: rfaD, probable ADP-L-glycero-mannoheptose epimerase

Nm1958: lgtF, β -1,4-glucosyltransferase

25 bp ahead Nm2135: sugar isomerase

Genes only present in serogroup B

NmB1771: hypothetical protein

NmB65: hypothetical protein

NmB1926: lgtE, lacto-N-neotetraose biosynthesis glycosyl transferase

received 13/06/02

D

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PATENT OF INVENTION
UTILITY CERTIFICATE
Intellectual property code – Book VI

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the sole inventor)

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APPLICANT(S):			
I.N.S.E.R.M.			
DESIGNATE(S) AS INVENTOR(S): (Indicate above right "Page No. 1/1. If there are more than three inventors, use an identical form and number each page indicating the total number of pages)."			
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First names		Vladimir	
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